

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:10:04 ; Search time 68.5294 Seconds
 (without alignments)
 202.471 Million cell updates/sec

Title: US-10-749-522-8
 Perfect score: 85
 Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB	ID
<hr/>					
1	51	60.0	849	2	Q54XC3_DICDI
2	47	55.3	1043	2	Q2NNR2_LEIBR
3	45	52.9	218	2	Q3K645_PSEPF
4	45	52.9	218	2	Q2XGZ9_PSEPU
5	45	52.9	345	2	Q4JWS4_CORJK
6	44.5	52.4	181	2	Q41EV6_9BACI
7	44.5	52.4	868	2	Q6K7N9_ORYSA
8	44.5	52.4	995	2	Q6K7P0_ORYSA
9	44	51.8	217	2	Q48DB5_PSE14
10	44	51.8	217	2	Q4ZMX7_PSEU2
11	44	51.8	266	2	Q8FSX8_COREF
12	44	51.8	519	2	Q2TW73_ASPOR
13	44	51.8	944	2	Q4UHB1_THEAN
14	44	51.8	2180	2	Q5B489_EMENI
15	43	50.6	292	2	Q568A9_BRARE

16	43	50.6	294	2	Q47TN4_THEFY	Q47tn4 thermobifid
17	43	50.6	325	2	Q58IN5_9ACTO	Q58in5 streptomyce
18	43	50.6	380	2	Q41SI9_FERAC	Q41si9 ferroplasma
19	43	50.6	433	2	Q5AY89_EMENI	Q5ay89 aspergillus
20	43	50.6	582	2	Q55N28_CRYNE	Q55n28 cryptococcu
21	43	50.6	582	2	Q5KBF7_CRYNE	Q5kbf7 cryptococcu
22	43	50.6	583	2	Q740E5_MYCPA	Q740e5 mycobacteri
23	43	50.6	586	1	PYRG_MYCBO	P0a5u3 mycobacteri
24	43	50.6	586	1	PYRG_MYCTU	P0a5u2 mycobacteri
25	43	50.6	605	2	Q65VA6_MANSM	Q65va6 mannheimia
26	43	50.6	636	2	Q3GI16_CHLVI	Q3gi16 prosthecoch
27	43	50.6	733	2	Q60JD4_CAEBR	Q60jd4 caenorhabdi
28	43	50.6	778	2	Q7QC12_ANOGA	Q7qc12 anopheles g
29	43	50.6	1358	2	Q30C85_9REOV	Q30c85 operophtera
30	42	49.4	87	2	Q650T0_ORYSA	Q650t0 oryza sativ
31	42	49.4	134	2	Q35C32_9BRAD	Q35c32 bradyrhizob
32	42	49.4	225	2	Q4TDL5_TETNG	Q4tdl5 tetraodon n
33	42	49.4	236	2	Q5QUS9_IDILO	Q5qus9 idiomarina
34	42	49.4	246	2	Q40NS7_DESAC	Q40ns7 desulfuromo
35	42	49.4	266	2	Q8NF60_HUMAN	Q8nf60 homo sapien
36	42	49.4	277	2	Q7UKR4_RHOBA	Q7ukr4 rhodopirell
37	42	49.4	298	2	Q82FC5_STRAW	Q82fc5 streptomyce
38	42	49.4	325	2	Q3F6Z1_9BURK	Q3f6z1 burkholderi
39	42	49.4	342	2	Q4SR00_TETNG	Q4sr00 tetraodon n
40	42	49.4	366	2	Q61FM3_CAEBR	Q61fm3 caenorhabdi
41	42	49.4	485	2	Q3KDP9_PSEPF	Q3kdp9 pseudomonas
42	42	49.4	502	2	Q6YZN3_ORYSA	Q6yzn3 oryza sativ
43	42	49.4	529	2	Q4E549_TRYCR	Q4e549 trypanosoma
44	42	49.4	781	2	Q440Z5_SOLUS	Q440z5 solibacter
45	42	49.4	841	2	Q2WRI3_CLOBE	Q2wri3 clostridium
46	42	49.4	935	2	Q5AXG4_EMENI	Q5axg4 aspergillus
47	42	49.4	939	2	Q4W9N5_ASPEFU	Q4w9n5 aspergillus
48	42	49.4	988	2	Q9P3H7_NEUCR	Q9p3h7 neurospora
49	42	49.4	1005	2	Q4IPN4_GIBZE	Q4ipn4 gibberella
50	42	49.4	1372	2	Q4I8F4_GIBZE	Q4i8f4 gibberella
51	41	48.2	145	2	Q4PEC5_USTMA	Q4pec5 ustilago ma
52	41	48.2	191	2	Q9C9T5_ARATH	Q9c9t5 arabidopsis
53	41	48.2	213	2	Q89GB2_BRAJA	Q89gb2 bradyrhizob
54	41	48.2	217	2	Q889R2_PSESM	Q889r2 pseudomonas
55	41	48.2	223	2	Q6M4J9_CORGL	Q6m4j9 corynebacte
56	41	48.2	239	2	Q8NPN2_CORGL	Q8npn2 corynebacte
57	41	48.2	255	2	Q8N9S2_HUMAN	Q8n9s2 homo sapien
58	41	48.2	266	2	Q8NL70_CORGL	Q8nl70 corynebacte
59	41	48.2	267	2	Q8Y296_RALSO	Q8y296 ralstonia s
60	41	48.2	271	2	Q6ABN5_PROAC	Q6abn5 propionibac

Search completed: August 14, 2006, 15:15:43
 Job time : 115.529 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:12:05 ; Search time 20 Seconds
 (without alignments)
 72.163 Million cell updates/sec

Title: US-10-749-522-8
 Perfect score: 85
 Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
		1	45	52.9	168	1	PAECGA	phosphatidylglycer
		2	43	50.6	586	2	B70503	probable pyrG prot
		3	42	49.4	988	2	T51054	related to alpha-a
		4	41	48.2	191	2	A96765	hypothetical prote
		5	41	48.2	298	2	H98170	myo-inositol catab
		6	41	48.2	298	2	AE3116	myo-inositol catab
		7	41	48.2	313	2	H87731	protein W10C8.1 [i
		8	41	48.2	622	2	S17402	parasporal crystal
		9	41	48.2	907	2	T04820	aconitase hydratas
		10	40	47.1	253	2	F84845	hypothetical prote
		11	40	47.1	816	2	S46268	ataxin-1 - human
		12	39	45.9	141	2	C83529	hypothetical prote
		13	39	45.9	142	2	T46542	hypothetical prote

14	39	45.9	280	2	B81100	2-dehydro-3-deoxyp
15	39	45.9	280	2	G81840	2-dehydro-3-deoxy-
16	39	45.9	316	2	B49702	hypothetical prote
17	39	45.9	359	2	A95277	hypothetical prote
18	39	45.9	424	1	HMIHCC	hemagglutinin-este
19	39	45.9	612	2	I73633	gene trkC protein
20	39	45.9	674	2	F82844	oligopeptidase A X
21	39	45.9	713	2	F82822	NADH-ubiquinone ox
22	39	45.9	898	2	T10101	aconitate hydratas
23	39	45.9	1488	2	T02856	probable membrane
24	38	44.7	180	2	C97050	phage related prot
25	38	44.7	214	2	S39831	hypothetical prote
26	38	44.7	233	2	C96709	hypothetical prote
27	38	44.7	263	2	T29199	hypothetical prote
28	38	44.7	420	2	D87545	cation efflux syst
29	38	44.7	440	2	H95373	probable NreB prot
30	38	44.7	513	2	AB2504	hypothetical prote
31	38	44.7	519	2	D82522	type I restriction
32	38	44.7	531	2	T44803	type I site-specif
33	38	44.7	531	2	T09460	type I site-specif
34	38	44.7	531	2	T30323	type I site-specif
35	38	44.7	633	2	D32053	parasporal crystal
36	38	44.7	704	2	S21911	BRcore-NS-Z3 prote
37	38	44.7	764	2	S49849	aconitate hydratas
38	38	44.7	905	2	T23229	hypothetical prote
39	38	44.7	1020	2	D83679	hypothetical prote
40	38	44.7	1201	2	G86441	unknown protein [i
41	37.5	44.1	1141	2	T05068	hypothetical prote
42	37.5	44.1	1165	2	T15279	hypothetical prote
43	37.5	44.1	1819	2	T26533	hypothetical prote
44	37	43.5	74	2	AH2331	50S ribosomal prot
45	37	43.5	149	1	GGWN2C	globin IIC, extrac
46	37	43.5	220	1	QQBE49	BALF1 protein - hu
47	37	43.5	222	2	AE3114	hypothetical prote
48	37	43.5	224	2	H84829	hypothetical prote
49	37	43.5	227	2	A95238	hypothetical prote
50	37	43.5	234	2	B98102	L-ribulose-phospha
51	37	43.5	244	2	JC7299	transformer-2-like
52	37	43.5	262	2	AB3545	toluenesulfonate z
53	37	43.5	269	2	T22443	hypothetical prote
54	37	43.5	270	2	H98172	amino acid ABC tra
55	37	43.5	314	2	G71974	probable keto-acid
56	37	43.5	314	2	H64531	phosphoglycerate d
57	37	43.5	336	2	T39669	probable cinnamoyl
58	37	43.5	374	2	AF1280	probable exonuclea
59	37	43.5	393	2	AG2246	hypothetical prote
60	37	43.5	404	2	C71538	hypothetical prote

Search completed: August 14, 2006, 15:16:57
 Job time : 41 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:20:06 ; Search time 17.9412 Seconds
 (without alignments)
 56.277 Million cell updates/sec

Title: US-10-749-522-8

Perfect score: 85

Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published_Applications_AA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	44.5	52.4	868	6	US-10-449-902-36512	Sequence 36512, A
2	42	49.4	502	6	US-10-449-902-54007	Sequence 54007, A
3	41	48.2	105	6	US-10-449-902-39504	Sequence 39504, A
4	41	48.2	454	6	US-10-449-902-29549	Sequence 29549, A
5	39	45.9	294	7	US-11-056-355B-64758	Sequence 64758, A
6	39	45.9	319	7	US-11-056-355B-64757	Sequence 64757, A
7	39	45.9	345	7	US-11-056-355B-64756	Sequence 64756, A
8	39	45.9	370	7	US-11-174-307B-2998	Sequence 2998, Ap
9	39	45.9	565	6	US-10-449-902-43212	Sequence 43212, A

10	38	44.7	146	7	US-11-056-355B-90573	Sequence 90573, A
11	38	44.7	146	7	US-11-056-355B-94329	Sequence 94329, A
12	38	44.7	227	7	US-11-375-414-136	Sequence 136, App
13	38	44.7	233	7	US-11-056-355B-90572	Sequence 90572, A
14	38	44.7	233	7	US-11-056-355B-94328	Sequence 94328, A
15	38	44.7	364	7	US-11-056-355B-2976	Sequence 2976, Ap
16	38	44.7	413	7	US-11-056-355B-2975	Sequence 2975, Ap
17	38	44.7	450	7	US-11-056-355B-2974	Sequence 2974, Ap
18	38	44.7	531	6	US-10-953-349-37173	Sequence 37173, A
19	38	44.7	1127	7	US-11-056-355B-46398	Sequence 46398, A
20	38	44.7	1191	7	US-11-056-355B-46397	Sequence 46397, A
21	38	44.7	1201	7	US-11-056-355B-46396	Sequence 46396, A
22	37.5	44.1	95	7	US-11-056-355B-57741	Sequence 57741, A
23	37.5	44.1	97	7	US-11-056-355B-57740	Sequence 57740, A
24	37.5	44.1	120	6	US-10-953-349-16348	Sequence 16348, A
25	37.5	44.1	190	6	US-10-953-349-16347	Sequence 16347, A
26	37.5	44.1	307	6	US-10-449-902-51738	Sequence 51738, A
27	37.5	44.1	586	6	US-10-449-902-52760	Sequence 52760, A
28	37	43.5	69	6	US-10-953-349-25347	Sequence 25347, A
29	37	43.5	73	6	US-10-953-349-25346	Sequence 25346, A
30	37	43.5	87	7	US-11-056-355B-7885	Sequence 7885, Ap
31	37	43.5	87	7	US-11-056-355B-11876	Sequence 11876, A
32	37	43.5	128	7	US-11-056-355B-7884	Sequence 7884, Ap
33	37	43.5	128	7	US-11-056-355B-11875	Sequence 11875, A
34	37	43.5	134	6	US-10-953-349-25345	Sequence 25345, A
35	37	43.5	192	6	US-10-953-349-1611	Sequence 1611, Ap
36	37	43.5	192	7	US-11-056-355B-38410	Sequence 38410, A
37	37	43.5	192	7	US-11-056-355B-103797	Sequence 103797,
38	37	43.5	192	7	US-11-056-355B-115036	Sequence 115036,
39	37	43.5	199	6	US-10-953-349-1610	Sequence 1610, Ap
40	37	43.5	199	7	US-11-056-355B-38409	Sequence 38409, A
41	37	43.5	199	7	US-11-056-355B-103796	Sequence 103796,
42	37	43.5	199	7	US-11-056-355B-115035	Sequence 115035,
43	37	43.5	223	6	US-10-449-902-34605	Sequence 34605, A
44	37	43.5	224	6	US-10-953-349-1609	Sequence 1609, Ap
45	37	43.5	224	7	US-11-056-355B-38408	Sequence 38408, A
46	37	43.5	224	7	US-11-056-355B-103795	Sequence 103795,
47	37	43.5	224	7	US-11-056-355B-115034	Sequence 115034,
48	37	43.5	271	7	US-11-056-355B-17214	Sequence 17214, A
49	37	43.5	287	6	US-10-449-902-32722	Sequence 32722, A
50	37	43.5	291	7	US-11-056-355B-17213	Sequence 17213, A
51	37	43.5	301	7	US-11-056-355B-8863	Sequence 8863, Ap
52	37	43.5	396	7	US-11-056-355B-17212	Sequence 17212, A
53	37	43.5	455	7	US-11-056-355B-50054	Sequence 50054, A
54	37	43.5	477	7	US-11-056-355B-50053	Sequence 50053, A
55	37	43.5	534	7	US-11-056-355B-13954	Sequence 13954, A
56	37	43.5	534	7	US-11-056-355B-18290	Sequence 18290, A
57	37	43.5	548	7	US-11-056-355B-13953	Sequence 13953, A
58	37	43.5	548	7	US-11-056-355B-18289	Sequence 18289, A
59	37	43.5	1148	7	US-11-247-437-6	Sequence 6, Appli
60	36.5	42.9	317	7	US-11-293-697-3930	Sequence 3930, Ap

Search completed: August 14, 2006, 15:25:02

Job time : 22.1912 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:19:11 ; Search time 74.4118 Seconds
 (without alignments)
 93.375 Million cell updates/sec

Title: US-10-749-522-8
 Perfect score: 85
 Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	85	100.0	15	3	US-09-808-037-8	Sequence 8, Appli
2	85	100.0	15	4	US-10-162-889-8	Sequence 8, Appli
3	85	100.0	15	4	US-10-384-788-8	Sequence 8, Appli
4	85	100.0	15	4	US-10-618-856-8	Sequence 8, Appli
5	85	100.0	15	4	US-10-622-087-89	Sequence 89, Appli
6	85	100.0	15	5	US-10-749-522-8	Sequence 8, Appli
7	85	100.0	15	6	US-11-073-526-8	Sequence 8, Appli
8	52	61.2	74	4	US-10-425-115-273531	Sequence 273531,
9	45	52.9	12	4	US-10-706-391-24	Sequence 24, Appli
10	45	52.9	12	4	US-10-706-391-25	Sequence 25, Appli
11	45	52.9	12	4	US-10-706-391-28	Sequence 28, Appli

12	45	52.9	267	5	US-10-450-763-54537	Sequence 54537, A
13	44.5	52.4	872	4	US-10-437-963-119587	Sequence 119587,
14	44	51.8	50	4	US-10-424-599-269977	Sequence 269977,
15	43	50.6	408	4	US-10-437-963-122937	Sequence 122937,
16	43	50.6	543	4	US-10-282-122A-62808	Sequence 62808, A
17	43	50.6	583	4	US-10-282-122A-61811	Sequence 61811, A
18	43	50.6	586	4	US-10-282-122A-64598	Sequence 64598, A
19	43	50.6	1148	4	US-10-259-194A-278	Sequence 278, App
20	43	50.6	1536	5	US-10-498-428-2	Sequence 2, Appl
21	43	50.6	1731	4	US-10-437-963-105727	Sequence 105727,
22	43	50.6	6238	4	US-10-343-710-71	Sequence 71, Appl
23	42	49.4	87	4	US-10-437-963-150467	Sequence 150467,
24	42	49.4	94	3	US-09-764-891-3085	Sequence 3085, Ap
25	42	49.4	94	4	US-10-205-428-271	Sequence 271, App
26	42	49.4	285	4	US-10-425-114-71586	Sequence 71586, A
27	42	49.4	285	4	US-10-425-115-321529	Sequence 321529,
28	42	49.4	298	4	US-10-156-761-11864	Sequence 11864, A
29	42	49.4	353	4	US-10-437-963-121434	Sequence 121434,
30	42	49.4	485	6	US-11-188-298-9870	Sequence 9870, Ap
31	42	49.4	502	4	US-10-437-963-169378	Sequence 169378,
32	42	49.4	634	6	US-11-067-557-168	Sequence 168, App
33	42	49.4	634	6	US-11-067-557-176	Sequence 176, App
34	42	49.4	885	4	US-10-433-802-8	Sequence 8, Appl
35	41	48.2	123	4	US-10-437-963-190370	Sequence 190370,
36	41	48.2	155	4	US-10-767-701-48753	Sequence 48753, A
37	41	48.2	190	4	US-10-425-114-50570	Sequence 50570, A
38	41	48.2	205	6	US-11-055-822-548	Sequence 548, App
39	41	48.2	205	6	US-11-055-822-1128	Sequence 1128, Ap
40	41	48.2	224	6	US-11-055-822-546	Sequence 546, App
41	41	48.2	224	6	US-11-055-822-1126	Sequence 1126, Ap
42	41	48.2	239	3	US-09-738-626-5459	Sequence 5459, Ap
43	41	48.2	255	4	US-10-104-047-3876	Sequence 3876, Ap
44	41	48.2	255	6	US-11-072-512-3876	Sequence 3876, Ap
45	41	48.2	266	3	US-09-738-626-6904	Sequence 6904, Ap
46	41	48.2	311	4	US-10-767-701-39873	Sequence 39873, A
47	41	48.2	357	4	US-10-425-114-69939	Sequence 69939, A
48	41	48.2	363	4	US-10-425-114-42461	Sequence 42461, A
49	41	48.2	384	4	US-10-425-115-219332	Sequence 219332,
50	41	48.2	401	4	US-10-425-114-50173	Sequence 50173, A
51	41	48.2	462	4	US-10-425-114-51448	Sequence 51448, A
52	41	48.2	517	4	US-10-437-963-106387	Sequence 106387,
53	41	48.2	573	4	US-10-425-114-40721	Sequence 40721, A
54	41	48.2	579	4	US-10-425-114-56872	Sequence 56872, A
55	41	48.2	579	4	US-10-425-115-216734	Sequence 216734,
56	41	48.2	625	4	US-10-428-961-48	Sequence 48, Appl
57	41	48.2	759	4	US-10-080-334-236	Sequence 236, App
58	41	48.2	764	4	US-10-080-334-80	Sequence 80, Appl
59	41	48.2	804	4	US-10-080-334-235	Sequence 235, App
60	41	48.2	834	4	US-10-176-306-11	Sequence 11, Appl

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:15:15 ; Search time 34.4118 Seconds
 (without alignments)
 38.154 Million cell updates/sec

Title: US-10-749-522-8
 Perfect score: 85
 Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	85	100.0	15	2	US-09-830-954A-8	Sequence 8, Appli
2	45	52.9	443	2	US-09-489-039A-10246	Sequence 10246, A
3	44	51.8	804	2	US-09-252-991A-21676	Sequence 21676, A
4	41	48.2	192	2	US-09-605-703B-2524	Sequence 2524, Ap
5	41	48.2	255	2	US-10-104-047-3876	Sequence 3876, Ap
6	41	48.2	353	2	US-09-252-991A-26103	Sequence 26103, A
7	41	48.2	431	2	US-09-489-039A-14276	Sequence 14276, A
8	41	48.2	623	2	US-09-041-991A-6	Sequence 6, Appli
9	41	48.2	623	2	US-09-608-533A-6	Sequence 6, Appli
10	41	48.2	625	2	US-09-661-322A-48	Sequence 48, Appli

11	41	48.2	633	2	US-09-041-991A-8	Sequence 8, Appli
12	41	48.2	633	2	US-09-041-991A-10	Sequence 10, Appli
13	41	48.2	633	2	US-09-608-533A-8	Sequence 8, Appli
14	41	48.2	633	2	US-09-608-533A-10	Sequence 10, Appli
15	41	48.2	1596	2	US-09-328-352-5542	Sequence 5542, Ap
16	40	47.1	273	2	US-09-252-991A-17447	Sequence 17447, A
17	40	47.1	314	2	US-09-248-796A-18946	Sequence 18946, A
18	40	47.1	659	2	US-09-252-991A-17731	Sequence 17731, A
19	40	47.1	789	2	US-10-207-706-5	Sequence 5, Appli
20	40	47.1	792	2	US-10-207-706-4	Sequence 4, Appli
21	40	47.1	816	1	US-08-267-803B-9	Sequence 9, Appli
22	40	47.1	816	2	US-09-041-886-17	Sequence 17, Appli
23	40	47.1	816	2	US-09-538-092-1208	Sequence 1208, Ap
24	40	47.1	816	2	US-10-207-706-3	Sequence 3, Appli
25	39	45.9	84	1	US-08-359-705B-41	Sequence 41, Appli
26	39	45.9	84	1	US-08-286-846A-41	Sequence 41, Appli
27	39	45.9	84	1	US-08-457-880A-41	Sequence 41, Appli
28	39	45.9	84	2	US-08-444-622A-41	Sequence 41, Appli
29	39	45.9	84	2	US-09-156-923-41	Sequence 41, Appli
30	39	45.9	149	2	US-09-252-991A-29051	Sequence 29051, A
31	39	45.9	612	1	US-08-359-705B-8	Sequence 8, Appli
32	39	45.9	612	1	US-08-286-846A-8	Sequence 8, Appli
33	39	45.9	612	1	US-08-457-880A-8	Sequence 8, Appli
34	39	45.9	612	2	US-08-444-622A-8	Sequence 8, Appli
35	39	45.9	612	2	US-08-942-562-8	Sequence 8, Appli
36	39	45.9	612	2	US-09-156-923-8	Sequence 8, Appli
37	39	45.9	1399	2	US-08-462-467B-14	Sequence 14, Appli
38	38	44.7	69	2	US-09-248-796A-24357	Sequence 24357, A
39	38	44.7	199	2	US-09-482-273-205	Sequence 205, App
40	38	44.7	227	2	US-09-774-639-155	Sequence 155, App
41	38	44.7	316	2	US-09-252-991A-27084	Sequence 27084, A
42	38	44.7	357	2	US-09-252-991A-32564	Sequence 32564, A
43	38	44.7	376	2	US-09-248-796A-19334	Sequence 19334, A
44	38	44.7	402	2	US-09-489-039A-12788	Sequence 12788, A
45	38	44.7	473	2	US-09-328-352-5279	Sequence 5279, Ap
46	38	44.7	609	2	US-09-252-991A-32547	Sequence 32547, A
47	38	44.7	633	2	US-09-186-002-18	Sequence 18, Appli
48	38	44.7	634	2	US-09-186-002-2	Sequence 2, Appli
49	38	44.7	2584	2	US-08-936-135-4	Sequence 4, Appli
50	38	44.7	2588	2	US-08-936-135-2	Sequence 2, Appli
51	38	44.7	3218	1	US-08-764-100-27	Sequence 27, Appli
52	37.5	44.1	458	2	US-10-029-180-100	Sequence 100, App
53	37	43.5	94	2	US-09-345-236B-15	Sequence 15, Appli
54	37	43.5	140	2	US-09-949-002-440	Sequence 440, App
55	37	43.5	215	2	US-09-252-991A-32685	Sequence 32685, A
56	37	43.5	234	2	US-09-583-110-4749	Sequence 4749, Ap
57	37	43.5	236	2	US-09-107-433-3704	Sequence 3704, Ap
58	37	43.5	242	2	US-09-902-540-16132	Sequence 16132, A
59	37	43.5	307	2	US-09-328-352-7631	Sequence 7631, Ap
60	37	43.5	308	2	US-09-265-585C-102	Sequence 102, App

Search completed: August 14, 2006, 15:18:35
 Job time : 48.4118 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:04:09 ; Search time 59.1176 Seconds
 (without alignments)
 116.010 Million cell updates/sec

Title: US-10-749-522-8

Perfect score: 85

Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
1	85	100.0	15	4	AAB47110	Aab47110 Epitope #
2	85	100.0	15	6	AAO16068	Aao16068 Neurologi
3	85	100.0	15	8	ADJ88115	Adj88115 fd phage
4	85	100.0	15	8	ADK52265	Adk52265 Amyloid b
5	46	54.1	54	4	AAU66289	Aau66289 Propionib
6	46	54.1	54	6	ABM62808	Abm62808 Propionib
7	46	54.1	101	4	AAU50750	Aau50750 Propionib

8	46	54.1	101	6	ABM47269	Abm47269 Propionib
9	46	54.1	446	7	ABM89892	Abm89892 Rice abio
10	45	52.9	12	8	ADQ15529	Adq15529 Targeting
11	45	52.9	12	8	ADQ15532	Adq15532 Targeting
12	45	52.9	12	8	ADQ15528	Adq15528 Targeting
13	45	52.9	267	4	ABG24178	Abg24178 Novel hum
14	45	52.9	443	7	ABO63729	Abo63729 Klebsiell
15	44.5	52.4	917	8	ADO62489	Ado62489 Transcrip
16	44.5	52.4	995	10	AEF11503	Aef11503 Rice meth
17	44	51.8	804	7	ABO72930	Abo72930 Pseudomon
18	43	50.6	322	9	AED14591	Aed14591 VSM-relat
19	43	50.6	543	6	ABU34884	Abu34884 Protein e
20	43	50.6	583	6	ABU33887	Abu33887 Protein e
21	43	50.6	586	6	ABU36674	Abu36674 Protein e
22	43	50.6	1148	8	ADI45347	Adi45347 Rice isop
23	42	49.4	88	5	ABB98895	Abb98895 ATP/GTP c
24	42	49.4	94	4	AAM94427	Aam94427 Human rep
25	42	49.4	94	4	ABB10765	Abb10765 Human ova
26	42	49.4	260	2	AAY50353	Aay50353 Human LOB
27	42	49.4	285	8	ADY23802	Ady23802 Plant ful
28	42	49.4	456	7	ABM88806	Abm88806 Rice abio
29	42	49.4	483	2	AAY50355	Aay50355 Human LOB
30	42	49.4	617	7	ADL22707	Adl22707 Human dis
31	42	49.4	634	9	AEC38987	Aec38987 Bacillus
32	42	49.4	634	9	AEC38979	Aec38979 Bacillus
33	42	49.4	885	5	AAE25384	Aae25384 Human NZM
34	41	48.2	190	8	ADX87906	Adx87906 Plant ful
35	41	48.2	192	9	AED72348	Aed72348 Corynebac
36	41	48.2	205	4	AAB80197	Aab80197 Corynebac
37	41	48.2	205	4	AAB79907	Aab79907 Corynebac
38	41	48.2	224	4	AAB79906	Aab79906 Corynebac
39	41	48.2	224	4	AAB80196	Aab80196 Corynebac
40	41	48.2	239	4	AAG91705	Aag91705 C glutami
41	41	48.2	255	7	ADB65722	Adb65722 Human pro
42	41	48.2	266	4	AAG93150	Aag93150 C glutami
43	41	48.2	294	4	AAU58127	Aau58127 Propionib
44	41	48.2	294	6	ABM54646	Abm54646 Propionib
45	41	48.2	328	3	AAB43187	Aab43187 Human ORF
46	41	48.2	353	7	ABO77357	Abo77357 Pseudomon
47	41	48.2	357	8	ADY14124	Ady14124 Plant ful
48	41	48.2	363	8	ADX73095	Adx73095 Plant ful
49	41	48.2	401	8	ADX87509	Adx87509 Plant ful
50	41	48.2	431	7	ABO67759	Abo67759 Klebsiell
51	41	48.2	462	8	ADX88784	Adx88784 Plant ful
52	41	48.2	573	8	ADX71355	Adx71355 Plant ful
53	41	48.2	579	8	ADX94208	Adx94208 Plant ful
54	41	48.2	623	2	AAW75773	Aaw75773 Amino aci
55	41	48.2	625	4	AAU02044	Aau02044 B. thurin
56	41	48.2	633	2	AAW75775	Aaw75775 Amino aci
57	41	48.2	633	2	AAW75774	Aaw75774 Amino aci
58	41	48.2	764	6	ABU52617	Abu52617 Human NOV
59	41	48.2	801	9	AEA19953	Aea19953 Novel hum
60	41	48.2	804	5	ABB97954	Abb97954 Human pro

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:10:04 ; Search time 27.4118 Seconds
 (without alignments)
 202.471 Million cell updates/sec

Title: US-10-749-522-7

Perfect score: 38

Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB	ID
<hr/>					
1	38	100.0	376	2	Q8N105_HUMAN
2	38	100.0	516	2	Q7Z5S7_HUMAN
3	38	100.0	543	2	Q5D0E6_HUMAN
4	38	100.0	543	2	Q86WY1_HUMAN
5	35	92.1	92	2	Q6BG37_PARTE
6	35	92.1	148	2	Q8KNG2_MICEC
7	35	92.1	154	2	Q84HP9_9ACTO
8	35	92.1	158	2	Q84HM8_9ACTO
9	35	92.1	158	2	Q84HN3_9ACTO
10	35	92.1	173	2	Q5HV09_CAMJR
11	35	92.1	174	2	Q9PPD6_CAMJE
12	35	92.1	202	2	Q4N3S3_THEPA
13	35	92.1	204	2	Q5LR70_SILPO
14	35	92.1	350	2	Q5FSE4_GLUOX
15	35	92.1	355	2	Q6TUE0_RAT

16	35	92.1	362	2	Q8K4B5_MOUSE	Q8k4b5 mus musculu
17	35	92.1	362	2	Q924S2_MOUSE	Q924s2 m 2',5'-oli
18	35	92.1	376	2	Q78ZX0_MOUSE	Q78zx0 mus musculu
19	35	92.1	376	2	Q8JZN0_MOUSE	Q8jzn0 mus musculu
20	35	92.1	376	2	Q8K4E9_MOUSE	Q8k4e9 mus musculu
21	35	92.1	376	2	Q921F0_MOUSE	Q921f0 mus musculu
22	35	92.1	467	2	O96421_DROME	O96421 drosophila
23	35	92.1	467	2	Q9VV72_DROME	Q9vv72 drosophila
24	35	92.1	479	2	Q3U178_MOUSE	Q3u178 mus musculu
25	35	92.1	536	2	Q8BRV6_MOUSE	Q8brv6 mus musculu
26	35	92.1	825	2	Q80VH0_MOUSE	Q80vh0 mus musculu
27	35	92.1	992	2	Q4A0Y6_STAS1	Q4a0y6 staphylococ
28	34	89.5	25	2	Q7R843_PLAYO	Q7r843 plasmodium
29	34	89.5	229	2	Q82KU7_STRAW	Q82ku7 streptomyce
30	34	89.5	315	2	Q8IDQ8_PLAF7	Q8idq8 plasmodium
31	34	89.5	361	2	Q95KH3_MACFA	Q95kh3 macaca fasc
32	34	89.5	409	2	Q2L3B1_BRASY	Q2l3b1 brachypodiu
33	34	89.5	431	2	Q2WB67_MAGSA	Q2wb67 magnetospir
34	34	89.5	469	2	Q8NBC8_HUMAN	Q8nbc8 homo sapien
35	34	89.5	575	2	Q6NT32_HUMAN	Q6nt32 homo sapien
36	34	89.5	654	2	Q36UQ1_MARHY	Q36uq1 marinobacte
37	33	86.8	89	2	Q7R9R9_PLAYO	Q7r9r9 plasmodium
38	33	86.8	186	2	Q2IMQ8_9DELT	Q2imq8 anaeromyxob
39	33	86.8	301	2	Q4DI15_TRYCR	Q4di15 trypanosoma
40	33	86.8	301	2	Q4DIH0_TRYCR	Q4dih0 trypanosoma
41	33	86.8	305	2	Q386B9_9TRYP	Q386b9 trypanosoma
42	33	86.8	329	2	Q369J6_9GAMM	Q369j6 shewanella
43	33	86.8	359	2	Q3VIU6_9CHLB	Q3viu6 pelodictyon
44	33	86.8	376	2	Q7PNU3_ANOGA	Q7pnu3 anopheles g
45	33	86.8	430	2	Q60424_CRIGR	Q60424 cricetulus
46	33	86.8	483	2	Q4YYH4_PLABE	Q4yyh4 plasmodium
47	33	86.8	580	2	Q60425_CRIGR	Q60425 cricetulus
48	33	86.8	610	2	Q3GE91_9FIRM	Q3ge91 syntrophomo
49	33	86.8	650	2	Q8EP63_OCEIH	Q8ep63 oceanobacil
50	33	86.8	698	2	Q6BGZ2_DEBHA	Q6bgz2 debaryomyce
51	33	86.8	700	2	Q2UQX1_ASPOR	Q2uqx1 aspergillus
52	33	86.8	757	2	Q4SII8_TETNG	Q4sii8 tetraodon n
53	33	86.8	794	2	Q60426_CRIGR	Q60426 cricetulus
54	33	86.8	814	2	Q76KC9_ORYLA	Q76kc9 oryzias lat
55	33	86.8	834	2	Q4S7D2_TETNG	Q4s7d2 tetraodon n
56	33	86.8	927	2	Q6LFU1_PHOPR	Q6lfu1 photobacter
57	33	86.8	979	2	Q3W9C6_9ACTO	Q3w9c6 frankia sp.
58	33	86.8	1780	2	Q4SQ87_TETNG	Q4sq87 tetraodon n
59	32	84.2	129	2	Q6SA76_9FABA	Q6sa76 vigna radia
60	32	84.2	154	2	Q84HL7_9ACTO	Q84hl7 streptomyce

Search completed: August 14, 2006, 15:17:02

Job time : 67.4118 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:12:05 ; Search time 8 Seconds
 (without alignments)
 72.163 Million cell updates/sec

Title: US-10-749-522-7

Perfect score: 38

Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB	ID
<hr/>					
1	35	92.1	174	2	G81349
2	32	84.2	394	2	T45085
3	32	84.2	395	2	B75047
4	32	84.2	397	2	A71114
5	32	84.2	404	2	C71907
6	32	84.2	425	2	H71167
7	32	84.2	506	2	G86806
8	32	84.2	600	2	T06775
9	32	84.2	600	2	T06420
10	32	84.2	731	2	S29870
11	31	81.6	73	2	A81071
12	31	81.6	73	2	E81061
13	31	81.6	306	2	G96990

14	31	81.6	338	2	T46981	hypothetical prote
15	31	81.6	338	2	AD0241	probable dehydroge
16	31	81.6	354	2	S15660	(2'-5')oligo(A) sy
17	31	81.6	358	2	S31407	(2'-5')oligo(A) sy
18	31	81.6	367	1	SYMS01	(2'-5')oligo(A) sy
19	31	81.6	387	2	B82891	ferrichrome transp
20	31	81.6	406	2	S17712	kdgC protein - Erw
21	31	81.6	572	2	S73541	phosphotransferase
22	31	81.6	581	1	S71170	phosphoinositide-s
23	31	81.6	581	2	T50841	phosphoinositide-s
24	31	81.6	634	2	AE2558	hypothetical prote
25	31	81.6	773	2	D86268	F13B4.3 protein -
26	31	81.6	1678	2	T35547	hypothetical prote
27	30	78.9	79	2	B36670	cell division cont
28	30	78.9	227	1	QQBEC9	HXLF4 protein prec
29	30	78.9	229	2	B70158	conserved hypothet
30	30	78.9	276	2	F90405	asparinase, probab
31	30	78.9	383	2	JC7507	45K WW domain-cont
32	30	78.9	386	2	S76193	hypothetical prote
33	30	78.9	386	2	JC7508	45K WW domain-cont
34	30	78.9	475	2	G90005	hypothetical prote
35	30	78.9	502	2	AD3563	erythritol-4-phosp
36	30	78.9	532	2	A34329	60K esterase (EC 3
37	30	78.9	557	2	A47162	thiolesterase B (E
38	30	78.9	559	1	JC5408	carboxylesterase (
39	30	78.9	561	2	S47655	carboxylesterase (
40	30	78.9	585	2	T07425	phosphoinositide-s
41	30	78.9	590	2	H70130	oligoendopeptidase
42	30	78.9	605	2	T50842	phospholipase C2 [
43	30	78.9	643	2	H83635	conserved hypothet
44	30	78.9	723	2	I39066	N-methyl-D-asparta
45	30	78.9	726	2	G83310	conserved hypothet
46	30	78.9	741	2	D83633	conserved hypothet
47	30	78.9	872	2	T41147	hypothetical prote
48	30	78.9	1170	2	S30010	probable finger pr
49	30	78.9	1482	2	I49704	glutamate receptor
50	30	78.9	1482	2	B43274	N-methyl-D-asparta
51	30	78.9	1484	2	S52086	N-methyl-D-asparta
52	30	78.9	1498	2	S78102	chitin synthase (E
53	30	78.9	2287	2	T21312	hypothetical prote
54	29	76.3	98	2	A82648	hypothetical prote
55	29	76.3	174	2	D83692	hypothetical prote
56	29	76.3	175	2	C90631	hypothetical prote
57	29	76.3	187	2	B83695	hypothetical prote
58	29	76.3	193	2	G83901	hypothetical prote
59	29	76.3	207	2	C85482	hypothetical prote
60	29	76.3	343	2	AE1146	hypothetical prote

Search completed: August 14, 2006, 15:17:25

Job time : 21 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:20:06 ; Search time 7.17647 Seconds
 (without alignments)
 56.277 Million cell updates/sec

Title: US-10-749-522-7

Perfect score: 38

Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
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1	34	89.5	413	7	US-11-056-355B-13110	Sequence 13110, A
2	34	89.5	435	7	US-11-056-355B-13109	Sequence 13109, A
3	34	89.5	463	7	US-11-056-355B-13108	Sequence 13108, A
4	32	84.2	186	6	US-10-953-349-22292	Sequence 22292, A
5	32	84.2	191	6	US-10-953-349-22291	Sequence 22291, A
6	32	84.2	225	6	US-10-953-349-28105	Sequence 28105, A
7	32	84.2	233	6	US-10-953-349-28104	Sequence 28104, A
8	32	84.2	275	6	US-10-953-349-28103	Sequence 28103, A
9	32	84.2	314	6	US-10-953-349-22290	Sequence 22290, A

10	32	84.2	894	7	US-11-330-403-18595	Sequence 18595, A
11	30	78.9	79	7	US-11-300-928-55	Sequence 55, Appl
12	30	78.9	86	6	US-10-953-349-22177	Sequence 22177, A
13	30	78.9	86	7	US-11-056-355B-57258	Sequence 57258, A
14	30	78.9	127	6	US-10-953-349-22176	Sequence 22176, A
15	30	78.9	127	7	US-11-056-355B-57257	Sequence 57257, A
16	30	78.9	170	6	US-10-449-902-48648	Sequence 48648, A
17	30	78.9	173	6	US-10-953-349-22175	Sequence 22175, A
18	30	78.9	173	7	US-11-056-355B-57256	Sequence 57256, A
19	30	78.9	446	6	US-10-449-902-42897	Sequence 42897, A
20	30	78.9	466	7	US-11-056-355B-38733	Sequence 38733, A
21	30	78.9	475	7	US-11-330-403-7676	Sequence 7676, Ap
22	30	78.9	481	6	US-10-471-571A-2194	Sequence 2194, Ap
23	30	78.9	486	7	US-11-056-355B-38732	Sequence 38732, A
24	30	78.9	491	7	US-11-056-355B-68168	Sequence 68168, A
25	30	78.9	493	7	US-11-056-355B-68167	Sequence 68167, A
26	30	78.9	501	6	US-10-449-902-45549	Sequence 45549, A
27	30	78.9	511	7	US-11-056-355B-68166	Sequence 68166, A
28	30	78.9	542	7	US-11-227-614-2	Sequence 2, Appli
29	30	78.9	542	7	US-11-227-614-4	Sequence 4, Appli
30	30	78.9	1480	7	US-11-339-440-10	Sequence 10, Appl
31	30	78.9	1480	7	US-11-339-452-10	Sequence 10, Appl
32	29	76.3	458	6	US-10-539-228-568	Sequence 568, App
33	29	76.3	764	7	US-11-330-403-12843	Sequence 12843, A
34	29	76.3	10625	7	US-11-330-403-1837	Sequence 1837, Ap
35	28	73.7	87	7	US-11-056-355B-7885	Sequence 7885, Ap
36	28	73.7	87	7	US-11-056-355B-11876	Sequence 11876, A
37	28	73.7	128	7	US-11-056-355B-7884	Sequence 7884, Ap
38	28	73.7	128	7	US-11-056-355B-11875	Sequence 11875, A
39	28	73.7	179	6	US-10-953-349-2300	Sequence 2300, Ap
40	28	73.7	179	7	US-11-056-355B-40233	Sequence 40233, A
41	28	73.7	179	7	US-11-056-355B-103778	Sequence 103778,
42	28	73.7	179	7	US-11-056-355B-115017	Sequence 115017,
43	28	73.7	209	6	US-10-953-349-2299	Sequence 2299, Ap
44	28	73.7	209	7	US-11-056-355B-40232	Sequence 40232, A
45	28	73.7	209	7	US-11-056-355B-103777	Sequence 103777,
46	28	73.7	209	7	US-11-056-355B-115016	Sequence 115016,
47	28	73.7	216	7	US-11-056-355B-103776	Sequence 103776,
48	28	73.7	216	7	US-11-056-355B-115015	Sequence 115015,
49	28	73.7	222	6	US-10-449-902-45603	Sequence 45603, A
50	28	73.7	251	6	US-10-449-902-42492	Sequence 42492, A
51	28	73.7	265	6	US-10-471-571A-1016	Sequence 1016, Ap
52	28	73.7	353	6	US-10-471-571A-176	Sequence 176, App
53	28	73.7	362	6	US-10-449-902-37167	Sequence 37167, A
54	28	73.7	492	6	US-10-449-902-51390	Sequence 51390, A
55	28	73.7	545	6	US-10-449-902-50416	Sequence 50416, A
56	28	73.7	674	7	US-11-056-355B-90660	Sequence 90660, A
57	28	73.7	674	7	US-11-056-355B-94416	Sequence 94416, A
58	28	73.7	674	7	US-11-330-403-273	Sequence 273, App
59	28	73.7	779	6	US-10-449-902-53491	Sequence 53491, A
60	28	73.7	997	6	US-10-449-902-41237	Sequence 41237, A

Search completed: August 14, 2006, 15:25:09

Job time : 10.4265 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:19:11 ; Search time 29.7647 Seconds
 (without alignments)
 93.375 Million cell updates/sec

Title: US-10-749-522-7

Perfect score: 38

Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
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1	38	100.0	6	3	US-09-808-037-7	Sequence 7, Appli
2	38	100.0	6	4	US-10-162-889-7	Sequence 7, Appli
3	38	100.0	6	4	US-10-384-788-7	Sequence 7, Appli
4	38	100.0	6	4	US-10-618-856-7	Sequence 7, Appli
5	38	100.0	6	4	US-10-622-087-90	Sequence 90, Appli
6	38	100.0	6	5	US-10-749-522-7	Sequence 7, Appli
7	38	100.0	6	6	US-11-073-526-7	Sequence 7, Appli
8	38	100.0	8	5	US-10-481-642-1	Sequence 1, Appli
9	38	100.0	376	4	US-10-104-047-3484	Sequence 3484, Ap
10	38	100.0	376	4	US-10-104-047-3532	Sequence 3532, Ap
11	38	100.0	376	6	US-11-072-512-3484	Sequence 3484, Ap

12	38	100.0	376	6	US-11-072-512-3532	Sequence 3532, Ap
13	38	100.0	516	4	US-10-144-194A-46	Sequence 46, Appl
14	38	100.0	516	5	US-10-491-566-46	Sequence 46, Appl
15	38	100.0	538	4	US-10-144-194A-48	Sequence 48, Appl
16	38	100.0	538	5	US-10-491-566-48	Sequence 48, Appl
17	38	100.0	543	4	US-10-144-194A-44	Sequence 44, Appl
18	38	100.0	543	5	US-10-491-566-44	Sequence 44, Appl
19	38	100.0	585	4	US-10-144-194A-50	Sequence 50, Appl
20	38	100.0	585	5	US-10-491-566-50	Sequence 50, Appl
21	35	92.1	148	4	US-10-152-886-15	Sequence 15, Appl
22	35	92.1	148	6	US-11-053-576-15	Sequence 15, Appl
23	35	92.1	148	6	US-11-053-052-15	Sequence 15, Appl
24	35	92.1	154	4	US-10-152-886-65	Sequence 65, Appl
25	35	92.1	154	6	US-11-053-576-65	Sequence 65, Appl
26	35	92.1	154	6	US-11-053-052-65	Sequence 65, Appl
27	35	92.1	158	4	US-10-152-886-55	Sequence 55, Appl
28	35	92.1	158	6	US-11-053-576-55	Sequence 55, Appl
29	35	92.1	158	6	US-11-053-052-55	Sequence 55, Appl
30	35	92.1	362	4	US-10-439-741-17	Sequence 17, Appl
31	35	92.1	362	6	US-11-012-762-30	Sequence 30, Appl
32	35	92.1	362	6	US-11-012-762-32	Sequence 32, Appl
33	35	92.1	376	4	US-10-439-741-14	Sequence 14, Appl
34	35	92.1	376	6	US-11-012-762-10	Sequence 10, Appl
35	35	92.1	376	6	US-11-012-762-16	Sequence 16, Appl
36	35	92.1	376	6	US-11-012-762-18	Sequence 18, Appl
37	35	92.1	376	6	US-11-012-762-40	Sequence 40, Appl
38	34	89.5	49	3	US-09-864-761-36376	Sequence 36376, A
39	34	89.5	174	4	US-10-767-701-39352	Sequence 39352, A
40	34	89.5	190	4	US-10-425-115-277065	Sequence 277065,
41	34	89.5	229	4	US-10-156-761-9803	Sequence 9803, Ap
42	34	89.5	273	4	US-10-767-701-44740	Sequence 44740, A
43	34	89.5	356	4	US-10-451-168-93	Sequence 93, Appl
44	34	89.5	356	5	US-10-980-387-93	Sequence 93, Appl
45	34	89.5	402	4	US-10-425-114-63108	Sequence 63108, A
46	34	89.5	433	4	US-10-425-115-277059	Sequence 277059,
47	34	89.5	433	6	US-11-087-099-4413	Sequence 4413, Ap
48	34	89.5	435	4	US-10-425-115-265195	Sequence 265195,
49	34	89.5	435	6	US-11-087-099-10693	Sequence 10693, A
50	34	89.5	453	4	US-10-425-115-277063	Sequence 277063,
51	34	89.5	453	4	US-10-425-115-277066	Sequence 277066,
52	34	89.5	453	6	US-11-087-099-4049	Sequence 4049, Ap
53	34	89.5	453	6	US-11-087-099-4060	Sequence 4060, Ap
54	34	89.5	457	6	US-11-087-099-4938	Sequence 4938, Ap
55	34	89.5	469	4	US-10-104-047-2219	Sequence 2219, Ap
56	34	89.5	469	6	US-11-072-512-2219	Sequence 2219, Ap
57	34	89.5	490	4	US-10-425-114-65418	Sequence 65418, A
58	34	89.5	507	4	US-10-425-114-66367	Sequence 66367, A
59	34	89.5	520	4	US-10-425-114-65206	Sequence 65206, A
60	34	89.5	575	4	US-10-451-168-91	Sequence 91, Appl

Search completed: August 14, 2006, 15:24:49

Job time : 46.7647 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:15:15 ; Search time 13.7647 Seconds
 (without alignments)
 38.154 Million cell updates/sec

Title: US-10-749-522-7

Perfect score: 38

Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Query				Description
	Score	Match	Length	DB ID	
<hr/>					
1	38	100.0	6	2 US-09-830-954A-7	Sequence 7, Appli
2	38	100.0	376	2 US-10-104-047-3484	Sequence 3484, Ap
3	38	100.0	376	2 US-10-104-047-3532	Sequence 3532, Ap
4	35	92.1	148	2 US-10-152-886-15	Sequence 15, Appl
5	35	92.1	154	2 US-10-152-886-65	Sequence 65, Appl
6	35	92.1	158	2 US-10-152-886-55	Sequence 55, Appl
7	34	89.5	469	2 US-10-104-047-2219	Sequence 2219, Ap
8	34	89.5	581	2 US-10-023-515-2.	Sequence 2, Appli
9	34	89.5	581	3 US-10-114-270-196	Sequence 196, App
10	33	86.8	94	2 US-09-902-540-10664	Sequence 10664, A

11	33	86.8	636	2	US-09-248-796A-14866	Sequence 14866, A
12	33	86.8	1180	2	US-09-543-681A-6436	Sequence 6436, Ap
13	32	84.2	88	2	US-09-270-767-33601	Sequence 33601, A
14	32	84.2	88	2	US-09-270-767-48818	Sequence 48818, A
15	32	84.2	154	2	US-10-152-886-85	Sequence 85, Appl
16	32	84.2	165	2	US-10-152-886-95	Sequence 95, Appl
17	32	84.2	502	1	US-08-960-022-10	Sequence 10, Appl
18	32	84.2	577	2	US-09-543-681A-8225	Sequence 8225, Ap
19	32	84.2	899	2	US-09-107-532A-4503	Sequence 4503, Ap
20	31	81.6	147	2	US-09-270-767-37924	Sequence 37924, A
21	31	81.6	147	2	US-09-270-767-53141	Sequence 53141, A
22	31	81.6	152	2	US-10-152-886-25	Sequence 25, Appl
23	31	81.6	153	2	US-10-152-886-35	Sequence 35, Appl
24	31	81.6	157	2	US-10-152-886-5	Sequence 5, Appl
25	31	81.6	162	2	US-10-152-886-3	Sequence 3, Appl
26	31	81.6	324	2	US-09-248-796A-20599	Sequence 20599, A
27	31	81.6	2175	2	US-09-693-205A-8	Sequence 8, Appl
28	31	81.6	3829	2	US-09-693-205A-2	Sequence 2, Appl
29	31	81.6	3829	2	US-09-693-205A-16	Sequence 16, Appl
30	31	81.6	3830	2	US-09-693-205A-4	Sequence 4, Appl
31	30	78.9	79	2	US-09-917-254-64	Sequence 64, Appl
32	30	78.9	110	2	US-09-949-016-9743	Sequence 9743, Ap
33	30	78.9	121	2	US-09-107-532A-5275	Sequence 5275, Ap
34	30	78.9	171	2	US-09-134-001C-5527	Sequence 5527, Ap
35	30	78.9	422	2	US-09-489-039A-12443	Sequence 12443, A
36	30	78.9	425	2	US-10-272-490-84	Sequence 84, Appl
37	30	78.9	449	2	US-10-272-490-18	Sequence 18, Appl
38	30	78.9	449	2	US-10-214-473-18	Sequence 18, Appl
39	30	78.9	457	2	US-09-902-540-11961	Sequence 11961, A
40	30	78.9	466	2	US-09-934-066-2	Sequence 2, Appl
41	30	78.9	488	2	US-09-134-001C-4246	Sequence 4246, Ap
42	30	78.9	542	3	US-10-233-933A-2	Sequence 2, Appl
43	30	78.9	542	3	US-10-233-933A-4	Sequence 4, Appl
44	30	78.9	559	2	US-09-595-682B-28	Sequence 28, Appl
45	30	78.9	559	2	US-09-949-016-6426	Sequence 6426, Ap
46	30	78.9	559	2	US-10-019-219-7	Sequence 7, Appl
47	30	78.9	559	3	US-09-622-568A-28	Sequence 28, Appl
48	30	78.9	571	2	US-10-036-041-23	Sequence 23, Appl
49	30	78.9	577	2	US-09-949-016-9670	Sequence 9670, Ap
50	30	78.9	650	2	US-09-252-991A-17330	Sequence 17330, A
51	30	78.9	749	2	US-09-252-991A-17331	Sequence 17331, A
52	30	78.9	779	2	US-09-252-991A-31290	Sequence 31290, A
53	30	78.9	1347	2	US-09-949-016-9603	Sequence 9603, Ap
54	30	78.9	1456	1	US-08-026-138E-8	Sequence 8, Appl
55	30	78.9	1480	2	US-09-922-011-10	Sequence 10, Appl
56	30	78.9	1482	1	US-08-026-138E-2	Sequence 2, Appl
57	30	78.9	1484	1	US-08-231-193A-56	Sequence 56, Appl
58	30	78.9	1484	1	US-08-486-273A-56	Sequence 56, Appl
59	30	78.9	1484	2	US-08-940-086A-56	Sequence 56, Appl
60	30	78.9	1484	2	US-08-940-035A-56	Sequence 56, Appl

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:04:09 ; Search time 23.6471 Seconds
 (without alignments)
 116.010 Million cell updates/sec

Title: US-10-749-522-7

Perfect score: 38

Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*

1: geneseqp1980s:*

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5: geneseqp2002s:*

6: geneseqp2003as:*

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8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query				Description
No.	Score	Match	Length	DB	ID
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1	38	100.0	6	4	AAB47109
2	38	100.0	6	6	AAO16067
3	38	100.0	6	8	ADJ88114
4	38	100.0	6	8	ADK52266
5	38	100.0	8	6	ABP70740
6	38	100.0	12	6	ABP70747
7	38	100.0	238	4	AAU23469

8	38	100.0	376	7	ADB65378	Adb65378 Human pro
9	38	100.0	376	7	ADB65330	Adb65330 Human pro
10	38	100.0	516	6	ABR58300	Abr58300 BCU0730B
11	38	100.0	538	6	ABR58301	Abr58301 BCU0730C
12	38	100.0	543	6	ABR58299	Abr58299 BCU0730A
13	38	100.0	585	6	ABR58302	Abr58302 BCU0730D
14	35	92.1	148	5	ABG97423	Abg97423 M. echino
15	35	92.1	148	9	AEB12619	Aeb12619 Thioester
16	35	92.1	148	9	AEC10212	Aec10212 M. echino
17	35	92.1	154	5	ABG97448	Abg97448 M. megal
18	35	92.1	154	9	AEB12669	Aeb12669 Thioester
19	35	92.1	154	9	AEC10262	Aec10262 Micromono
20	35	92.1	158	5	ABG97443	Abg97443 Kitasatos
21	35	92.1	158	9	AEB12659	Aeb12659 Thioester
22	35	92.1	158	9	AEC10252	Aec10252 Kitasatos
23	35	92.1	362	8	ADJ34669	Adj34669 2'-5' oly
24	35	92.1	362	8	ADJ34668	Adj34668 Mouse 2'
25	35	92.1	362	8	ADI32343	Adi32343 Mouse OAS
26	35	92.1	376	8	ADJ34673	Adj34673 Mouse 2'
27	35	92.1	376	8	ADJ34661	Adj34661 Mouse BRV
28	35	92.1	376	8	ADJ34658	Adj34658 Mouse 2'
29	35	92.1	376	8	ADJ34662	Adj34662 Mouse MOL
30	35	92.1	376	8	ADI32340	Adi32340 Mouse OAS
31	34	89.5	49	4	AAM16665	Aam16665 Peptide #
32	34	89.5	49	4	ABB35649	Abb35649 Peptide #
33	34	89.5	49	4	AAM29149	Aam29149 Peptide #
34	34	89.5	49	4	ABB30482	Abb30482 Peptide #
35	34	89.5	49	4	ABB21078	Abb21078 Protein #
36	34	89.5	49	4	AAM68842	Aam68842 Human bon
37	34	89.5	49	4	AAM56465	Aam56465 Human bra
38	34	89.5	49	4	ABG50502	Abg50502 Human liv
39	34	89.5	49	4	AAM04381	Aam04381 Peptide #
40	34	89.5	49	5	ABG38423	Abg38423 Human pep
41	34	89.5	224	7	ADC55524	Adc55524 Human car
42	34	89.5	356	5	ABP61006	Abp61006 Novel hum
43	34	89.5	402	8	ADY07293	Ady07293 Plant ful
44	34	89.5	469	7	ADB64065	Adb64065 Human pro
45	34	89.5	490	8	ADY09603	Ady09603 Plant ful
46	34	89.5	507	8	ADY10552	Ady10552 Plant ful
47	34	89.5	520	8	ADY09391	Ady09391 Plant ful
48	34	89.5	575	5	ABP61004	Abp61004 Novel hum
49	34	89.5	581	5	ABP61005	Abp61005 Novel hum
50	34	89.5	581	5	ABB79537	Abb79537 Human car
51	34	89.5	581	6	ABU54639	Abu54639 Human NOV
52	34	89.5	581	8	ADQ89094	Adq89094 Human uro
53	34	89.5	618	5	ADR19663	Adr19663 Human dru
54	34	89.5	642	5	AAE25025	Aae25025 Human dru
55	34	89.5	642	8	ABM84114	Abm84114 Human dia
56	33	86.8	10	6	ABP70743	Abp70743 Antigenic
57	33	86.8	14	6	ABP70748	Abp70748 Antigenic
58	33	86.8	94	9	ABM91465	Abm91465 M. xanthu
59	33	86.8	1180	7	ADF06151	Adf06151 Bacterial
60	32	84.2	154	5	ABG97458	Abg97458 S. kaniha
61	32	84.2	154	9	AEB12689	Aeb12689 Thioester
62	32	84.2	154	9	AEC10282	Aec10282 Streptomy
63	32	84.2	165	5	ABG97463	Abg97463 S. citric
64	32	84.2	165	9	AEB12699	Aeb12699 Thioester

65	32	84.2	165	9	AEC10292	Aec10292 Streptomy
66	32	84.2	379	8	ADX68618	Adx68618 Plant ful
67	32	84.2	395	4	AAB96540	Aab96540 Putative
68	32	84.2	398	8	ADN47159	Adn47159 Thermococ
69	32	84.2	425	8	ADS41882	Ads41882 Bacterial
70	32	84.2	425	8	ADN18592	Adn18592 Bacterial
71	32	84.2	427	8	ADX88777	Adx88777 Plant ful
72	32	84.2	502	2	AAW80398	Aaw80398 A secrete
73	32	84.2	506	5	ABB54798	Abb54798 Lactococc
74	32	84.2	532	8	ADN47587	Adn47587 Thermococ
75	32	84.2	577	7	ADF07940	Adf07940 Bacterial
76	32	84.2	609	8	ADY04744	Ady04744 Plant ful
77	32	84.2	616	7	ADC32948	Adc32948 Human nov
78	32	84.2	616	7	ADF60299	Adf60299 Human con
79	32	84.2	666	4	ABB66873	Abb66873 Drosophil
80	32	84.2	666	4	ABB58867	Abb58867 Drosophil
81	32	84.2	731	7	ADK63252	Adk63252 Disease t
82	32	84.2	899	7	ADC94876	Adc94876 E. faeciu
83	31	81.6	6	8	ADQ82436	Adq82436 N-termina
84	31	81.6	6	10	AEF40969	Aef40969 N-termina
85	31	81.6	6	10	AEF40938	Aef40938 N-termina
86	31	81.6	7	10	AEF40929	Aef40929 N-termina
87	31	81.6	124	4	AAO05817	Aao05817 Human pol
88	31	81.6	152	5	ABG97428	Abg97428 S. ghanae
89	31	81.6	152	9	AEB12629	Aeb12629 Thioester
90	31	81.6	152	9	AEC10222	Aec10222 Streptomy
91	31	81.6	153	5	ABG97433	Abg97433 S. carzin
92	31	81.6	153	9	AEB12639	Aeb12639 Thioester
93	31	81.6	153	9	AEC10232	Aec10232 S. carzin
94	31	81.6	157	5	ABG97418	Abg97418 S. macrom
95	31	81.6	157	9	AEB12609	Aeb12609 Thioester
96	31	81.6	157	9	AEC10202	Aec10202 Streptomy
97	31	81.6	162	5	ABG97417	Abg97417 S. macrom
98	31	81.6	162	9	AEB12607	Aeb12607 Thioester
99	31	81.6	162	9	AEC10200	Aec10200 Streptomy
100	31	81.6	173	3	AAG25437	Aag25437 Arabidops

Search completed: August 14, 2006, 15:09:51
 Job time : 55.6471 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:10:04 ; Search time 68.5294 Seconds
 (without alignments)
 202.471 Million cell updates/sec

Title: US-10-749-522-22
 Perfect score: 84
 Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				Description
No.	Score	Match	Length	DB	ID
<hr/>					
1	47	56.0	219	2	Q7SHR7_NEUCR
2	46.5	55.4	3298	2	Q9VB11_DROME
3	46	54.8	169	2	Q59V02_CANAL
4	45	53.6	126	2	Q6R9H1_MAIZE
5	45	53.6	640	2	Q7RGH6_PLAYO
6	44	52.4	302	2	Q5TQQ5_ANOGA
7	44	52.4	308	2	Q5TX76_ANOGA
8	44	52.4	505	2	Q6ZN07_HUMAN
9	44	52.4	609	1	GLMS_IDILO
10	44	52.4	678	2	Q2UES9_ASPOR
11	44	52.4	691	2	Q43MD7_SOLUS
12	44	52.4	2423	2	Q5CQJ6_CRYPTSPORI
13	43.5	51.8	304	1	Y245_SYNYY3
14	43.5	51.8	681	1	PRZ1_SCHPO
15	43	51.2	119	2	Q3FX29_9BURK

16	43	51.2	297	2	Q5LY65_STRT1	Q5ly65 streptococc
17	43	51.2	297	2	Q5M2S0_STRT2	Q5m2s0 streptococc
18	43	51.2	394	2	Q3BNS1_XANC5	Q3bns1 xanthomonas
19	43	51.2	523	2	Q3E2F3_CHLAU	Q3e2f3 chloroflexu
20	43	51.2	610	2	Q3CSC7_ALTAT	Q3csc7 pseudoalter
21	43	51.2	901	2	Q7RWJ4_NEUCR	Q7rwj4 neurospora
22	43	51.2	906	2	Q45BS1_9BURK	Q45bs1 burkholderi
23	43	51.2	906	2	Q4LKD0_9BURK	Q41kd0 burkholderi
24	43	51.2	1323	2	Q4XZK4_PLACH	Q4xzk4 plasmodium
25	43	51.2	1896	2	Q4QJ26_LEIMA	Q4qj26 leishmania
26	43	51.2	4427	2	Q7X0P4_LACFE	Q7x0p4 lactobacill
27	42.5	50.6	2408	2	Q9V549_DROME	Q9v549 drosophila
28	42	50.0	55	2	Q3L8S5_SACKO	Q3l8s5 saccoglossu
29	42	50.0	195	2	Q5SW35_MOUSE	Q5sw35 mus musculu
30	42	50.0	208	2	Q3PWN9_NITHA	Q3pwn9 nitrobacter
31	42	50.0	255	2	Q3QVC4_9RHOB	Q3qvc4 silicibacte
32	42	50.0	271	2	Q4AHQ2_9CHLB	Q4ahq2 chlorobium
33	42	50.0	310	2	Q2T100_BURTH	Q2t100 burkholderi
34	42	50.0	329	2	Q2PRK3_BRARE	Q2prk3 brachydanio
35	42	50.0	475	1	UAP1_SCHPO	O94617 schizosacch
36	42	50.0	596	2	Q3TZN3_MOUSE	Q3tzn3 mus musculu
37	42	50.0	657	1	ACSA_CAMJE	Q9pmd2 campylobact
38	42	50.0	657	2	Q4HDX0_CAMCO	Q4hdx0 campylobact
39	42	50.0	657	2	Q5HSP9_CAMJR	Q5hsp9 campylobact
40	42	50.0	678	2	Q7QUM5_GIALA	Q7qum5 giardia lam
41	42	50.0	893	2	Q5SW34_MOUSE	Q5sw34 mus musculu
42	42	50.0	903	2	Q3TK98_MOUSE	Q3tk98 mus musculu
43	42	50.0	907	2	Q5SW33_MOUSE	Q5sw33 mus musculu
44	42	50.0	914	1	ZFP62_MOUSE	Q8c827 mus musculu
45	42	50.0	914	2	Q3U3H0_MOUSE	Q3u3h0 mus musculu
46	42	50.0	1182	2	Q4N9F0_THEPA	Q4n9f0 theileria p
47	42	50.0	1512	2	Q7XPJ2_ORYSA	Q7xpj2 oryza sativ
48	42	50.0	1625	2	Q4SZD8_TETNG	Q4szd8 tetraodon n
49	42	50.0	7059	1	R1AB_CVBQ	Q8v6w7 b replicase
50	42	50.0	7094	1	R1AB_CVBEN	Q91a29 b replicase
51	42	50.0	7094	1	R1AB_CVBLU	Q8v439 b replicase
52	42	50.0	7094	1	R1AB_CVBM	Q66198 b replicase
53	42	50.0	7095	2	Q2QKN6_9CORS	Q2qkn6 porcine hem
54	42	50.0	7095	2	Q4VID8_CVHOC	Q4vid8 human coron
55	42	50.0	7095	2	Q4VIE7_CVHOC	Q4vie7 human coron
56	42	50.0	7095	2	Q696Q1_CVHOC	Q696q1 human coron
57	42	50.0	7095	2	Q6TNG2_CVHOC	Q6tng2 human coron
58	41.5	49.4	195	1	DCD_HALMA	Q5v1d1 haloarcula
59	41.5	49.4	555	2	Q55ZL9_CRYNE	Q55zl9 cryptococcu
60	41.5	49.4	658	2	Q4WR79_ASPEFU	Q4wr79 aspergillus

Search completed: August 14, 2006, 15:16:22

Job time : 107.529 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:12:05 ; Search time 20 Seconds
 (without alignments)
 72.163 Million cell updates/sec

Title: US-10-749-522-22
 Perfect score: 84
 Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB	ID
<hr/>					
1	43.5	51.8	304	1	S74557
2	43.5	51.8	681	2	S62490
3	42	50.0	475	2	T39359
4	42	50.0	657	2	G81300
5	41.5	49.4	706	2	A82091
6	41	48.8	345	2	D84089
7	41	48.8	436	2	S48399
8	41	48.8	460	2	T45968
9	41	48.8	609	2	JC4258
10	40.5	48.2	249	2	AB2039
11	40.5	48.2	316	2	G82204
12	40.5	48.2	1391	2	T20642
13	40.5	48.2	1397	2	E87998

14	40	47.6	330	2	T31704	hypothetical prote
15	40	47.6	605	2	S16561	glutamine-fructose
16	40	47.6	608	1	S01040	glutamine-fructose
17	40	47.6	608	2	B95322	NodM Glutamine ami
18	40	47.6	746	2	G84605	hypothetical prote
19	39	46.4	339	2	T26328	hypothetical prote
20	39	46.4	482	2	S69580	hypothetical prote
21	39	46.4	523	2	D86284	F9L1.1 protein - A
22	39	46.4	606	2	E87263	hypothetical prote
23	39	46.4	1039	2	T22982	hypothetical prote
24	39	46.4	1076	2	T30842	serine-repeat anti
25	39	46.4	1159	2	B95370	probable adenylate
26	39	46.4	1192	2	H88293	protein F59B10.1 [
27	39	46.4	2626	2	T31099	myosin-RhoGAP prot
28	38.5	45.8	295	2	F69976	conserved hypothet
29	38	45.2	207	2	B71446	hypothetical prote
30	38	45.2	294	2	E69817	hypothetical prote
31	38	45.2	305	2	T52299	squamosa promoter
32	38	45.2	311	1	QQBEC1	HKLF1 protein - hu
33	38	45.2	367	2	G71803	hypothetical prote
34	38	45.2	467	2	G82081	UDP-N-acetylmuramo
35	38	45.2	496	2	S58300	probable excision
36	38	45.2	526	2	S46766	hypothetical prote
37	38	45.2	609	2	AB0500	glutamine-fructose
38	38	45.2	629	2	A30168	homeotic protein L
39	38	45.2	726	2	T51519	cyclic nucleotide-
40	38	45.2	825	2	S62042	probable membrane
41	38	45.2	1802	2	S69703	HKR1 protein precu
42	38	45.2	2140	2	T18543	probable cell-adhe
43	37	44.0	109	2	A83934	hypothetical prote
44	37	44.0	222	2	AE2191	hypothetical prote
45	37	44.0	299	2	AB1776	hypothetical prote
46	37	44.0	338	2	F82358	lysophospholipase
47	37	44.0	351	2	E97187	dTDP-D-glucose 4,6
48	37	44.0	385	2	S49752	homeotic protein Y
49	37	44.0	419	2	H81667	transcription term
50	37	44.0	464	2	A71509	probable transcrip
51	37	44.0	518	1	XYIMHA	homoserine O-acetyl
52	37	44.0	519	2	H86897	gluconokinase (EC
53	37	44.0	536	2	S40717	hypothetical prote
54	37	44.0	559	2	F96500	hypothetical prote
55	37	44.0	643	2	B71848	probable outer mem
56	37	44.0	710	2	T22360	hypothetical prote
57	37	44.0	748	1	S08680	methylmalonyl-CoA
58	37	44.0	750	1	A59145	methylmalonyl-CoA
59	37	44.0	788	2	S53923	probable membrane
60	37	44.0	863	2	S06017	neuraxin - rat

Search completed: August 14, 2006, 15:17:12
 Job time : 35 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:20:06 ; Search time 17.9412 Seconds
 (without alignments)
 56.277 Million cell updates/sec

Title: US-10-749-522-22
 Perfect score: 84
 Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	43	51.2	264	7	US-11-317-789A-719	Sequence 719, App
2	42.5	50.6	316	7	US-11-056-355B-55593	Sequence 55593, A
3	42.5	50.6	338	7	US-11-056-355B-55592	Sequence 55592, A
4	42.5	50.6	349	7	US-11-056-355B-55591	Sequence 55591, A
5	42	50.0	315	7	US-11-056-355B-5101	Sequence 5101, Ap
6	42	50.0	635	7	US-11-056-355B-72152	Sequence 72152, A
7	42	50.0	710	7	US-11-056-355B-72151	Sequence 72151, A
8	42	50.0	710	7	US-11-056-355B-86609	Sequence 86609, A
9	41	48.8	308	6	US-10-953-349-26736	Sequence 26736, A

10	40	47.6	170	6	US-10-449-902-41030	Sequence 41030, A
11	40	47.6	258	7	US-11-056-355B-16289	Sequence 16289, A
12	40	47.6	448	7	US-11-174-307B-3428	Sequence 3428, Ap
13	40	47.6	473	7	US-11-056-355B-16288	Sequence 16288, A
14	40	47.6	508	7	US-11-056-355B-16287	Sequence 16287, A
15	39	46.4	575	7	US-11-056-355B-44632	Sequence 44632, A
16	39	46.4	575	7	US-11-056-355B-76951	Sequence 76951, A
17	39	46.4	578	7	US-11-056-355B-44631	Sequence 44631, A
18	39	46.4	578	7	US-11-056-355B-76950	Sequence 76950, A
19	39	46.4	729	7	US-11-121-133-268	Sequence 268, App
20	38.5	45.8	262	6	US-10-449-902-41759	Sequence 41759, A
21	38	45.2	127	6	US-10-953-349-13146	Sequence 13146, A
22	38	45.2	149	6	US-10-953-349-13145	Sequence 13145, A
23	38	45.2	179	6	US-10-953-349-13144	Sequence 13144, A
24	38	45.2	209	6	US-10-953-349-867	Sequence 867, App
25	38	45.2	209	7	US-11-056-355B-28617	Sequence 28617, A
26	38	45.2	209	7	US-11-056-355B-29397	Sequence 29397, A
27	38	45.2	209	7	US-11-056-355B-32207	Sequence 32207, A
28	38	45.2	209	7	US-11-056-355B-32987	Sequence 32987, A
29	38	45.2	209	7	US-11-056-355B-91370	Sequence 91370, A
30	38	45.2	209	7	US-11-056-355B-95126	Sequence 95126, A
31	38	45.2	222	7	US-11-056-355B-16655	Sequence 16655, A
32	38	45.2	249	7	US-11-317-789A-517	Sequence 517, App
33	38	45.2	249	7	US-11-317-789A-518	Sequence 518, App
34	38	45.2	289	6	US-10-953-349-866	Sequence 866, App
35	38	45.2	289	7	US-11-056-355B-28616	Sequence 28616, A
36	38	45.2	289	7	US-11-056-355B-29396	Sequence 29396, A
37	38	45.2	289	7	US-11-056-355B-32206	Sequence 32206, A
38	38	45.2	289	7	US-11-056-355B-32986	Sequence 32986, A
39	38	45.2	289	7	US-11-056-355B-91369	Sequence 91369, A
40	38	45.2	289	7	US-11-056-355B-95125	Sequence 95125, A
41	38	45.2	289	7	US-11-056-355B-108600	Sequence 108600,
42	38	45.2	289	7	US-11-056-355B-119839	Sequence 119839,
43	38	45.2	361	7	US-11-056-355B-91368	Sequence 91368, A
44	38	45.2	361	7	US-11-056-355B-95124	Sequence 95124, A
45	38	45.2	373	6	US-10-953-349-865	Sequence 865, App
46	38	45.2	373	7	US-11-113-081A-2	Sequence 2, Appli
47	38	45.2	373	7	US-11-056-355B-28615	Sequence 28615, A
48	38	45.2	373	7	US-11-056-355B-29395	Sequence 29395, A
49	38	45.2	373	7	US-11-056-355B-32205	Sequence 32205, A
50	38	45.2	373	7	US-11-056-355B-32985	Sequence 32985, A
51	38	45.2	373	7	US-11-056-355B-108599	Sequence 108599,
52	38	45.2	373	7	US-11-056-355B-119838	Sequence 119838,
53	38	45.2	389	7	US-11-056-355B-108598	Sequence 108598,
54	38	45.2	389	7	US-11-056-355B-119837	Sequence 119837,
55	38	45.2	439	6	US-10-953-349-19898	Sequence 19898, A
56	38	45.2	498	7	US-11-056-355B-79485	Sequence 79485, A
57	38	45.2	525	7	US-11-056-355B-79484	Sequence 79484, A
58	38	45.2	2304	6	US-10-540-898-310	Sequence 310, App
59	37.5	44.6	851	6	US-10-540-898-397	Sequence 397, App
60	37	44.0	34	7	US-11-223-610-56	Sequence 56, Appl

Search completed: August 14, 2006, 15:25:06

Job time : 22.1912 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:19:11 ; Search time 74.4118 Seconds
 (without alignments)
 93.375 Million cell updates/sec

Title: US-10-749-522-22
 Perfect score: 84
 Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
<hr/>						
1	84	100.0	15	3	US-09-808-037-22	Sequence 22, Appl
2	84	100.0	15	4	US-10-162-889-22	Sequence 22, Appl
3	84	100.0	15	4	US-10-384-788-22	Sequence 22, Appl
4	84	100.0	15	4	US-10-618-856-22	Sequence 22, Appl
5	84	100.0	15	5	US-10-749-522-22	Sequence 22, Appl
6	84	100.0	15	6	US-11-073-526-22	Sequence 22, Appl
7	59	70.2	335	4	US-10-437-963-177702	Sequence 177702,
8	46.5	55.4	126	4	US-10-424-599-236661	Sequence 236661,
9	46	54.8	227	4	US-10-425-114-55911	Sequence 55911, A
10	46	54.8	305	4	US-10-437-963-143406	Sequence 143406,
11	46	54.8	377	4	US-10-424-599-241171	Sequence 241171,

12	45	53.6	81	4	US-10-437-963-124802	Sequence 124802,
13	45	53.6	642	4	US-10-437-963-140313	Sequence 140313,
14	44	52.4	83	4	US-10-437-963-192253	Sequence 192253,
15	44	52.4	180	4	US-10-437-963-111252	Sequence 111252,
16	43.5	51.8	304	6	US-11-087-099-10045	Sequence 10045, A
17	43	51.2	128	4	US-10-425-115-354458	Sequence 354458,
18	43	51.2	626	6	US-11-188-298-22376	Sequence 22376, A
19	43	51.2	901	6	US-11-087-099-1818	Sequence 1818, Ap
20	42.5	50.6	316	6	US-11-096-568A-3300	Sequence 3300, Ap
21	42.5	50.6	338	6	US-11-096-568A-3299	Sequence 3299, Ap
22	42.5	50.6	349	6	US-11-096-568A-3298	Sequence 3298, Ap
23	42.5	50.6	543	4	US-10-425-114-51382	Sequence 51382, A
24	42.5	50.6	570	4	US-10-424-599-156730	Sequence 156730,
25	42	50.0	61	4	US-10-425-115-310263	Sequence 310263,
26	42	50.0	61	4	US-10-425-115-364223	Sequence 364223,
27	42	50.0	85	4	US-10-424-599-143717	Sequence 143717,
28	42	50.0	100	4	US-10-425-115-339083	Sequence 339083,
29	42	50.0	159	4	US-10-437-963-188976	Sequence 188976,
30	42	50.0	577	4	US-10-029-180-48	Sequence 48, Appl
31	42	50.0	577	5	US-10-952-045-48	Sequence 48, Appl
32	42	50.0	635	6	US-11-096-568A-29628	Sequence 29628, A
33	42	50.0	657	4	US-10-282-122A-54608	Sequence 54608, A
34	42	50.0	710	6	US-11-096-568A-29627	Sequence 29627, A
35	42	50.0	1243	4	US-10-437-963-124960	Sequence 124960,
36	42	50.0	1512	4	US-10-437-963-181358	Sequence 181358,
37	41.5	49.4	706	4	US-10-282-122A-77432	Sequence 77432, A
38	41	48.8	60	4	US-10-425-115-296073	Sequence 296073,
39	41	48.8	100	4	US-10-437-963-106615	Sequence 106615,
40	41	48.8	144	4	US-10-424-599-239420	Sequence 239420,
41	41	48.8	247	6	US-11-182-480-57	Sequence 57, Appl
42	41	48.8	247	6	US-11-182-480-58	Sequence 58, Appl
43	41	48.8	247	6	US-11-182-408-57	Sequence 57, Appl
44	41	48.8	247	6	US-11-182-408-58	Sequence 58, Appl
45	41	48.8	295	5	US-10-898-775-4	Sequence 4, Appli
46	41	48.8	295	5	US-10-898-775-5	Sequence 5, Appli
47	41	48.8	295	5	US-10-911-160-4	Sequence 4, Appli
48	41	48.8	295	5	US-10-911-160-5	Sequence 5, Appli
49	41	48.8	295	6	US-11-182-480-4	Sequence 4, Appli
50	41	48.8	295	6	US-11-182-480-5	Sequence 5, Appli
51	41	48.8	295	6	US-11-182-408-4	Sequence 4, Appli
52	41	48.8	295	6	US-11-182-408-5	Sequence 5, Appli
53	41	48.8	1583	4	US-10-437-963-190592	Sequence 190592,
54	40.5	48.2	155	4	US-10-424-599-205115	Sequence 205115,
55	40	47.6	65	4	US-10-425-115-258104	Sequence 258104,
56	40	47.6	112	4	US-10-437-963-147941	Sequence 147941,
57	40	47.6	139	4	US-10-425-115-205443	Sequence 205443,
58	40	47.6	145	5	US-10-450-763-52419	Sequence 52419, A
59	40	47.6	180	4	US-10-424-599-234183	Sequence 234183,
60	40	47.6	186	4	US-10-425-115-255363	Sequence 255363,

Search completed: August 14, 2006, 15:24:32

Job time : 90.4118 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:15:15 ; Search time 34.4118 Seconds
 (without alignments)
 38.154 Million cell updates/sec

Title: US-10-749-522-22
 Perfect score: 84
 Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	84	100.0	15	2	US-09-830-954A-22	Sequence 22, Appl
2	51	60.7	656	2	US-09-902-540-9810	Sequence 9810, Ap
3	46	54.8	192	2	US-09-248-796A-26839	Sequence 26839, A
4	43	51.2	940	2	US-09-328-352-8165	Sequence 8165, Ap
5	42	50.0	577	2	US-10-029-180-48	Sequence 48, Appl
6	42	50.0	708	2	US-09-489-039A-10131	Sequence 10131, A
7	40	47.6	315	2	US-09-248-796A-18003	Sequence 18003, A
8	39.5	47.0	800	2	US-09-949-016-7703	Sequence 7703, Ap
9	39.5	47.0	947	2	US-09-418-780A-1	Sequence 1, Appli
10	39.5	47.0	947	2	US-09-392-714-23	Sequence 23, Appl

11	39	46.4	315	2	US-09-248-796A-23418	Sequence 23418, A
12	39	46.4	317	2	US-09-248-796A-26237	Sequence 26237, A
13	39	46.4	403	2	US-09-270-767-44912	Sequence 44912, A
14	39	46.4	455	2	US-09-270-767-35242	Sequence 35242, A
15	39	46.4	455	2	US-09-270-767-50459	Sequence 50459, A
16	39	46.4	729	1	US-08-971-937-2	Sequence 2, Appli
17	39	46.4	729	1	US-08-812-533-2	Sequence 2, Appli
18	39	46.4	729	2	US-09-771-161A-268	Sequence 268, App
19	39	46.4	749	2	US-09-949-016-10745	Sequence 10745, A
20	38	45.2	103	2	US-09-621-976-6639	Sequence 6639, Ap
21	38	45.2	276	2	US-09-270-767-32903	Sequence 32903, A
22	38	45.2	276	2	US-09-270-767-48120	Sequence 48120, A
23	38	45.2	331	2	US-09-252-991A-24420	Sequence 24420, A
24	38	45.2	345	2	US-09-489-039A-9471	Sequence 9471, Ap
25	38	45.2	395	2	US-09-252-991A-30497	Sequence 30497, A
26	38	45.2	492	2	US-09-710-279-1276	Sequence 1276, Ap
27	38	45.2	503	2	US-09-134-001C-3457	Sequence 3457, Ap
28	38	45.2	1456	2	US-09-949-016-9853	Sequence 9853, Ap
29	38	45.2	1891	1	US-08-804-227C-12	Sequence 12, Appl
30	38	45.2	1891	1	US-08-804-198-6	Sequence 6, Appli
31	37.5	44.6	322	2	US-09-328-352-4547	Sequence 4547, Ap
32	37.5	44.6	515	2	US-09-107-532A-6749	Sequence 6749, Ap
33	37	44.0	62	2	US-09-134-001C-4983	Sequence 4983, Ap
34	37	44.0	77	2	US-09-513-999C-4965	Sequence 4965, Ap
35	37	44.0	150	2	US-09-596-377A-33	Sequence 33, Appl
36	37	44.0	243	2	US-09-248-796A-14531	Sequence 14531, A
37	37	44.0	246	2	US-09-248-796A-18240	Sequence 18240, A
38	37	44.0	252	2	US-09-270-767-44627	Sequence 44627, A
39	37	44.0	335	2	US-09-252-991A-26591	Sequence 26591, A
40	37	44.0	412	2	US-09-902-540-15047	Sequence 15047, A
41	37	44.0	545	2	US-09-134-000C-3545	Sequence 3545, Ap
42	37	44.0	585	2	US-09-107-532A-4126	Sequence 4126, Ap
43	37	44.0	668	2	US-09-252-991A-22794	Sequence 22794, A
44	37	44.0	736	2	US-09-949-016-7488	Sequence 7488, Ap
45	37	44.0	739	2	US-08-510-646B-33	Sequence 33, Appl
46	37	44.0	819	2	US-09-543-681A-7385	Sequence 7385, Ap
47	37	44.0	820	2	US-09-328-352-5766	Sequence 5766, Ap
48	37	44.0	820	2	US-09-489-039A-12169	Sequence 12169, A
49	37	44.0	924	2	US-09-248-796A-18798	Sequence 18798, A
50	37	44.0	1014	2	US-09-492-709A-266	Sequence 266, App
51	37	44.0	1038	2	US-09-215-569B-12	Sequence 12, Appl
52	36.5	43.5	234	2	US-09-270-767-45995	Sequence 45995, A
53	36.5	43.5	303	2	US-09-270-767-45675	Sequence 45675, A
54	36.5	43.5	1085	2	US-09-198-452A-961	Sequence 961, App
55	36.5	43.5	1087	2	US-09-438-185A-893	Sequence 893, App
56	36	42.9	24	2	US-08-838-413A-27	Sequence 27, Appl
57	36	42.9	24	2	US-09-355-581-27	Sequence 27, Appl
58	36	42.9	84	2	US-09-489-847-147	Sequence 147, App
59	36	42.9	109	2	US-09-513-999C-5688	Sequence 5688, Ap
60	36	42.9	124	2	US-09-513-999C-5276	Sequence 5276, Ap

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:04:09 ; Search time 59.1176 Seconds
 (without alignments)
 116.010 Million cell updates/sec

Title: US-10-749-522-22
 Perfect score: 84
 Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	84	100.0	15	4	AAB47117	Aab47117 EFRH cont
2	84	100.0	15	6	AAO16077	Aao16077 Neurologi
3	84	100.0	15	8	ADJ88128	Adj88128 Anti-aggr
4	51	60.7	656	9	ABM90611	Abm90611 M. xanthu
5	46	54.8	227	8	ADX93247	Adx93247 Plant ful
6	44	52.4	185	5	ABP66058	Abp66058 Bifidobac
7	44	52.4	505	8	ADQ67682	Adq67682 Novel hum

8	43	51.2	156	4	ABB15642	Abb15642 Human ner
9	43	51.2	940	6	ADA36878	Ada36878 Acinetoba
10	42.5	50.6	543	8	ADX88718	Adx88718 Plant ful
11	42	50.0	577	5	ABP63107	Abp63107 FLO11 gen
12	42	50.0	657	6	ABU26684	Abu26684 Protein e
13	42	50.0	708	7	ABO63614	Abo63614 Klebsiell
14	42	50.0	7094	8	ABY03145	Aby03145 Bovine co
15	41.5	49.4	706	6	ABU49508	Abu49508 Protein e
16	41.5	49.4	706	8	ADR31327	Adr31327 Aspergill
17	41	48.8	295	8	ADR41617	Adr41617 Lipid acy
18	41	48.8	295	8	ADR41618	Adr41618 Lipid acy
19	41	48.8	295	8	ADR41567	Adr41567 Lipid acy
20	41	48.8	295	8	ADR41568	Adr41568 Lipid acy
21	41	48.8	295	9	AEB44070	Aeb44070 Lipid acy
22	41	48.8	295	9	AEB44069	Aeb44069 Lipid acy
23	41	48.8	295	9	AEB28310	Aeb28310 Glycolipi
24	41	48.8	295	9	AEB28311	Aeb28311 Glycolipi
25	41	48.8	295	10	AEF62807	Aef62807 Lipid acy
26	41	48.8	295	10	AEF62806	Aef62806 Lipid acy
27	40	47.6	50	5	ABP09600	Abp09600 Human ORF
28	40	47.6	77	4	AAO05814	Aao05814 Human pol
29	40	47.6	121	8	ADR09989	Adr09989 Human pro
30	40	47.6	145	4	ABG22060	Abg22060 Novel hum
31	40	47.6	191	8	ADX76729	Adx76729 Plant ful
32	40	47.6	395	7	ADB70108	Adb70108 C. neofor
33	40	47.6	473	4	ABB71149	Abb71149 Drosophil
34	40	47.6	553	6	ABR40771	Abr40771 Glycine m
35	40	47.6	607	8	ADS23171	Ads23171 Bacterial
36	40	47.6	629	8	ADS42606	Ads42606 Bacterial
37	39.5	47.0	124	4	ABG11004	Abg11004 Novel hum
38	39.5	47.0	233	4	ABG03905	Abg03905 Novel hum
39	39.5	47.0	324	9	AED96153	Aed96153 Human C-r
40	39.5	47.0	452	5	AAU79412	Aau79412 Human tra
41	39.5	47.0	528	4	AAB98977	Aab98977 Human PCL
42	39.5	47.0	528	6	ABU03462	Abu03462 Angiogene
43	39.5	47.0	528	8	ADI82178	Adi82178 Human pod
44	39.5	47.0	528	8	ADO44007	Ado44007 Amino aci
45	39.5	47.0	528	8	ADR70488	Adr70488 Human pod
46	39.5	47.0	528	9	ADV41988	Adv41988 Human pod
47	39.5	47.0	528	9	AED96152	Aed96152 Human C-r
48	39.5	47.0	528	9	AED96151	Aed96151 Human C-r
49	39.5	47.0	947	2	AAW81168	Aaw81168 Transcrip
50	39.5	47.0	947	2	AAY07114	Aay07114 WO9904265
51	39.5	47.0	947	8	ADJ96674	Adj96674 Human aty
52	39.5	47.0	947	8	ADJ54137	Adj54137 Human bro
53	39	46.4	26	4	ABG59772	Abg59772 Human liv
54	39	46.4	50	4	AAU48924	Aau48924 Propionib
55	39	46.4	50	6	ABM45443	Abm45443 Propionib
56	39	46.4	56	4	AAU61706	Aau61706 Propionib
57	39	46.4	56	6	ABM58225	Abm58225 Propionib
58	39	46.4	66	5	ABP08718	Abp08718 Human ORF
59	39	46.4	112	4	AAU86535	Aau86535 Novel hum
60	39	46.4	112	7	ADB59869	Adb59869 Connectiv

Search completed: August 14, 2006, 15:09:19

Job time : 94.1176 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:10:04 ; Search time 68.5294 Seconds
 (without alignments)
 202.471 Million cell updates/sec

Title: US-10-749-522-21
 Perfect score: 78
 Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%				Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	44	56.4	1100	2	Q5KF71_CRYNE	Q5kf71 cryptococco
2	44	56.4	1127	2	Q55QZ7_CRYNE	Q55qz7 cryptococco
3	43	55.1	1421	2	Q7QPX0_GIALA	Q7qpx0 giardia lam
4	42	53.8	112	2	Q4AC56_9SPHN	Q4ac56 sphingomona
5	42	53.8	190	2	Q80S36_9VIRU	Q80s36 mayaro viru
6	42	53.8	342	2	Q82DV3_STRAW	Q82dv3 streptomyce
7	42	53.8	394	2	Q4S539_TETNG	Q4s539 tetraodon n
8	42	53.8	530	2	Q61Q18_CAEBR	Q61q18 caenorhabdi
9	42	53.8	628	2	Q22015_CAEEL	Q22015 caenorhabdi
10	42	53.8	1121	2	Q9AKN9_RICMO	Q9akn9 rickettsia
11	42	53.8	2437	2	Q8QZ73_9VIRU	Q8qz73 mayaro viru
12	41	52.6	23	1	IAPP_LEPEU	Q07333 lepus europ
13	41	52.6	67	1	IAPP_RABIT	Q07334 oryctolagus
14	41	52.6	89	1	IAPP_HUMAN	P10997 homo sapien
15	41	52.6	112	2	Q5GRF6_ALCXX	Q5grf6 alcaligenes

16	41	52.6	112	2	Q8RSJ8_9BACT	Q8rsj8 uncultured
17	41	52.6	113	2	P71177_ENTAE	P71177 enterobacte
18	41	52.6	113	2	Q2VLE6_BURCE	Q2vle6 burkholderi
19	41	52.6	113	2	Q56467_9ZZZZ	Q56467 plasmid r75
20	41	52.6	113	2	Q6UP65_RALEJ	Q6up65 ralstonia e
21	41	52.6	113	2	Q76M42_COMAC	Q76m42 comamonas a
22	41	52.6	113	2	Q79BP5_PSESD	Q79bp5 pseudomonas
23	41	52.6	113	2	Q7BHY8_COMTE	Q7bhy8 comamonas t
24	41	52.6	113	2	Q7X3A2_9BACT	Q7x3a2 uncultured
25	41	52.6	113	2	Q3F2F0_9BURK	Q3f2f0 burkholderi
26	41	52.6	113	2	Q4LCG0_9ZZZZ	Q4lcg0 incp-1beta
27	41	52.6	113	2	Q5W3K4_9ZZZZ	Q5w3k4 plasmid pb3
28	41	52.6	117	2	Q87K58_VIBPA	Q87k58 vibrio para
29	41	52.6	161	2	Q7PB85_RICSI	Q7pb85 rickettsia
30	41	52.6	182	2	Q4UKR0_RICFE	Q4ukr0 rickettsia
31	41	52.6	184	2	Q92IR8_RICCN	Q92ir8 rickettsia
32	41	52.6	323	2	Q4XGF4_PLACH	Q4xgf4 plasmodium
33	41	52.6	363	1	Y2500_AGRT5	P58759 agrobacteri
34	41	52.6	476	2	Q4N593_THEPA	Q4n593 theileria p
35	41	52.6	527	2	Q4PB46_USTMA	Q4pb46 ustilago ma
36	41	52.6	670	2	Q7S6G9_NEUCR	Q7s6g9 neurospora
37	41	52.6	760	2	Q8I8Y0_MANSE	Q8i8y0 manduca sex
38	41	52.6	805	2	Q5A287_CANAL	Q5a287 candida alb
39	41	52.6	808	2	Q5A2D8_CANAL	Q5a2d8 candida alb
40	41	52.6	931	1	STE13 YEAST	P33894 saccharomyc
41	40	51.3	193	2	Q40IL2_EHRCH	Q40il2 ehrlichia c
42	40	51.3	279	2	Q5F759_NEIG1	Q5f759 neisseria g
43	40	51.3	279	2	Q9JT84_NEIMA	Q9jt84 neisseria m
44	40	51.3	279	2	Q9JYA2_NEIMB	Q9jya2 neisseria m
45	40	51.3	285	2	Q70GH8_NEISU	Q70gh8 neisseria s
46	40	51.3	350	2	Q2P7K9_XANOR	Q2p7k9 xanthomonas
47	40	51.3	350	2	Q5H4T4_XANOR	Q5h4t4 xanthomonas
48	40	51.3	411	2	Q965X2_CAEEL	Q965x2 caenorhabdi
49	40	51.3	411	2	Q965X3_CAEEL	Q965x3 caenorhabdi
50	40	51.3	469	2	Q8GUA8_MEDTR	Q8gua8 medicago tr
51	40	51.3	488	2	Q8XUR6_RALSO	Q8xur6 ralstonia s
52	40	51.3	717	2	Q4SR34_TETNG	Q4sr34 tetraodon n
53	40	51.3	720	1	EXO84_KLULA	Q6cnm8 kluyveromyc
54	40	51.3	814	2	Q52984_ECOLI	Q52984 escherichia
55	40	51.3	834	2	Q92LD3_RHIME	Q92ld3 rhizobium m
56	40	51.3	958	1	K6PF2_YEAST	P16862 saccharomyc
57	40	51.3	1161	2	Q57UJ3_9TRYP	Q57uj3 trypanosoma
58	40	51.3	1517	2	Q59DW9_DROME	Q59dw9 drosophila
59	40	51.3	1517	2	Q6XK18_DROME	Q6xk18 drosophila
60	40	51.3	2645	2	Q6XK19_DROME	Q6xk19 drosophila
61	40	51.3	3044	2	Q63CQ6_BACCZ	Q63cq6 bacillus ce
62	39	50.0	116	1	SPT4H_DROME	Q9tvq5 drosophila
63	39	50.0	193	2	Q07246_YEAST	Q07246 saccharomyc
64	39	50.0	203	2	Q2JE42_9ACTO	Q2je42 frankia sp.
65	39	50.0	229	2	Q3FKW1_9BURK	Q3fkwl rhodoferax

Search completed: August 14, 2006, 15:14:56
 Job time : 120.529 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:12:05 ; Search time 20 Seconds
 (without alignments)
 72.163 Million cell updates/sec

Title: US-10-749-522-21
 Perfect score: 78
 Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB	ID
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1	42	53.8	628	2	T24241
2	41	52.6	23	2	I46933
3	41	52.6	23	2	I46934
4	41	52.6	89	1	TCHUIA
5	41	52.6	113	2	T08497
6	41	52.6	184	2	H97743
7	41	52.6	318	2	AI2883
8	41	52.6	363	2	G97659
9	41	52.6	931	2	A49737
10	40	51.3	279	2	G81054
11	40	51.3	279	2	F81821
12	40	51.3	959	1	JQ0017
13	39	50.0	193	4	S59326

14	39	50.0	373	2	S52635	1-aminocyclopropan
15	39	50.0	526	2	AH0601	probable membrane
16	39	50.0	582	2	S10099	transcription fact
17	39	50.0	654	2	A34734	transcription fact
18	39	50.0	742	4	C34734	transcription fact
19	39	50.0	825	4	B34734	transcription fact
20	38	48.7	184	2	D71681	hypothetical prote
21	38	48.7	235	2	S69757	hypothetical prote
22	38	48.7	340	2	T21805	hypothetical prote
23	38	48.7	433	2	AC2275	hypothetical prote
24	38	48.7	436	2	A37953	transcription regu
25	38	48.7	638	2	B35816	transcription regu
26	38	48.7	649	1	B37953	transcription regu
27	38	48.7	649	2	A35816	transcription regu
28	38	48.7	835	2	T15177	hypothetical prote
29	38	48.7	1108	2	T17455	translation initia
30	38	48.7	1122	2	A97814	transcription-repa
31	38	48.7	1583	2	S59644	sister chromatid c
32	37.5	48.1	303	2	S71185	splicing factor SF
33	37.5	48.1	303	2	F86158	alternative splici
34	37	47.4	190	2	AH2216	nitrate transport
35	37	47.4	266	2	C84963	extragenic suppres
36	37	47.4	289	2	AH0484	conserved hypothet
37	37	47.4	296	2	T31582	hypothetical prote
38	37	47.4	327	2	T25780	hypothetical prote
39	37	47.4	401	2	T25784	hypothetical prote
40	37	47.4	427	1	S63615	malF protein homol
41	37	47.4	450	2	AF1884	glycolate oxidase
42	37	47.4	484	2	G72395	alpha-L-arabinofur
43	37	47.4	540	2	T47858	hypothetical prote
44	37	47.4	744	2	C90089	hypothetical prote
45	37	47.4	762	2	T14815	hypothetical prote
46	37	47.4	1028	2	G96769	unknown protein F9
47	37	47.4	1092	2	S42798	fibronectin-bindin
48	37	47.4	1117	2	S33851	fibronectin-bindin
49	37	47.4	1218	2	T29915	hypothetical prote
50	37	47.4	2957	2	T33152	hypothetical prote
51	36.5	46.8	411	2	S46800	LAG1 protein - yea
52	36.5	46.8	489	2	C75269	hypothetical prote
53	36	46.2	116	2	S07258	helix-destabilizin
54	36	46.2	201	2	E82695	hypothetical prote
55	36	46.2	230	2	AC0474	conserved hypothet
56	36	46.2	234	2	S14469	asparagine-rich pr
57	36	46.2	247	2	H82348	hypothetical prote
58	36	46.2	294	2	T33931	hypothetical prote
59	36	46.2	301	2	AH0649	conserved hypothet
60	36	46.2	378	2	AG1313	hypothetical prote

Search completed: August 14, 2006, 15:16:36
 Job time : 47 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:20:06 ; Search time 17.9412 Seconds
 (without alignments)
 56.277 Million cell updates/sec

Title: US-10-749-522-21
 Perfect score: 78
 Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
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1	47	60.3	28	6	US-10-890-071-53	Sequence 53, Appl
2	42	53.8	157	7	US-11-293-697-3717	Sequence 3717, Ap
3	41	52.6	35	7	US-11-055-093-211	Sequence 211, App
4	41	52.6	36	6	US-10-559-595-255	Sequence 255, App
5	41	52.6	36	7	US-11-055-093-68	Sequence 68, Appl
6	41	52.6	36	7	US-11-055-093-77	Sequence 77, Appl
7	41	52.6	36	7	US-11-055-093-210	Sequence 210, App
8	41	52.6	37	6	US-10-559-595-249	Sequence 249, App
9	41	52.6	37	6	US-10-559-595-256	Sequence 256, App

10	41	52.6	37	6	US-10-559-595-282	Sequence 282, App
11	41	52.6	37	6	US-10-559-595-283	Sequence 283, App
12	41	52.6	37	6	US-10-559-595-284	Sequence 284, App
13	41	52.6	37	6	US-10-559-595-285	Sequence 285, App
14	41	52.6	37	6	US-10-559-595-289	Sequence 289, App
15	41	52.6	37	7	US-11-055-093-45	Sequence 45, Appl
16	41	52.6	37	7	US-11-055-093-76	Sequence 76, Appl
17	41	52.6	37	7	US-11-055-093-78	Sequence 78, Appl
18	41	52.6	37	7	US-11-055-093-79	Sequence 79, Appl
19	41	52.6	37	7	US-11-055-093-80	Sequence 80, Appl
20	41	52.6	37	7	US-11-055-093-81	Sequence 81, Appl
21	41	52.6	37	7	US-11-055-093-82	Sequence 82, Appl
22	41	52.6	37	7	US-11-055-093-189	Sequence 189, App
23	40	51.3	469	7	US-11-330-403-1651	Sequence 1651, Ap
24	40	51.3	959	7	US-11-330-403-3471	Sequence 3471, Ap
25	40	51.3	959	7	US-11-330-403-4782	Sequence 4782, Ap
26	39	50.0	462	6	US-10-953-349-33642	Sequence 33642, A
27	39	50.0	477	6	US-10-953-349-33641	Sequence 33641, A
28	39	50.0	511	6	US-10-953-349-33640	Sequence 33640, A
29	38.5	49.4	715	7	US-11-056-355B-74169	Sequence 74169, A
30	38.5	49.4	718	7	US-11-056-355B-79095	Sequence 79095, A
31	38.5	49.4	719	7	US-11-056-355B-107994	Sequence 107994,
32	38.5	49.4	719	7	US-11-056-355B-119233	Sequence 119233,
33	37.5	48.1	147	7	US-11-056-355B-77122	Sequence 77122, A
34	37.5	48.1	165	7	US-11-056-355B-29319	Sequence 29319, A
35	37.5	48.1	165	7	US-11-056-355B-30964	Sequence 30964, A
36	37.5	48.1	165	7	US-11-056-355B-32909	Sequence 32909, A
37	37.5	48.1	165	7	US-11-056-355B-34554	Sequence 34554, A
38	37.5	48.1	285	7	US-11-056-355B-77121	Sequence 77121, A
39	37.5	48.1	303	7	US-11-056-355B-30963	Sequence 30963, A
40	37.5	48.1	303	7	US-11-056-355B-34553	Sequence 34553, A
41	37.5	48.1	307	7	US-11-056-355B-29318	Sequence 29318, A
42	37.5	48.1	307	7	US-11-056-355B-32908	Sequence 32908, A
43	37	47.4	36	6	US-10-559-595-288	Sequence 288, App
44	37	47.4	37	6	US-10-559-595-260	Sequence 260, App
45	37	47.4	37	7	US-11-055-093-69	Sequence 69, Appl
46	37	47.4	37	7	US-11-055-093-75	Sequence 75, Appl
47	37	47.4	805	6	US-10-449-902-55324	Sequence 55324, A
48	36	46.2	19	7	US-11-134-871-246	Sequence 246, App
49	36	46.2	36	6	US-10-559-595-263	Sequence 263, App
50	36	46.2	36	6	US-10-559-595-287	Sequence 287, App
51	36	46.2	36	7	US-11-055-093-74	Sequence 74, Appl
52	36	46.2	36	7	US-11-055-093-84	Sequence 84, Appl
53	36	46.2	37	6	US-10-559-595-257	Sequence 257, App
54	36	46.2	37	6	US-10-559-595-286	Sequence 286, App
55	36	46.2	37	6	US-10-559-595-290	Sequence 290, App
56	36	46.2	37	7	US-11-055-093-67	Sequence 67, Appl
57	36	46.2	37	7	US-11-055-093-83	Sequence 83, Appl
58	36	46.2	37	7	US-11-055-093-92	Sequence 92, Appl
59	36	46.2	37	7	US-11-244-135A-7	Sequence 7, Appli
60	36	46.2	329	6	US-10-953-349-13415	Sequence 13415, A

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:19:11 ; Search time 74.4118 Seconds
 (without alignments)
 93.375 Million cell updates/sec

Title: US-10-749-522-21
 Perfect score: 78
 Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	78	100.0	15	3	US-09-808-037-21	Sequence 21, Appl
2	78	100.0	15	4	US-10-162-889-21	Sequence 21, Appl
3	78	100.0	15	4	US-10-384-788-21	Sequence 21, Appl
4	78	100.0	15	4	US-10-618-856-21	Sequence 21, Appl
5	78	100.0	15	5	US-10-749-522-21	Sequence 21, Appl
6	78	100.0	15	6	US-11-073-526-21	Sequence 21, Appl
7	47	60.3	28	4	US-10-699-517-35	Sequence 35, Appl
8	47	60.3	28	4	US-10-698-099-35	Sequence 35, Appl
9	47	60.3	28	5	US-10-889-999-53	Sequence 53, Appl
10	47	60.3	28	5	US-10-890-070-53	Sequence 53, Appl
11	47	60.3	28	5	US-10-890-000-53	Sequence 53, Appl

12	47	60.3	28	5	US-10-823-463-53	Sequence 53, Appl
13	47	60.3	28	5	US-10-915-214-35	Sequence 35, Appl
14	47	60.3	28	5	US-10-822-968-53	Sequence 53, Appl
15	47	60.3	28	5	US-10-777-792-53	Sequence 53, Appl
16	47	60.3	28	5	US-10-890-071-53	Sequence 53, Appl
17	47	60.3	28	5	US-10-890-024-53	Sequence 53, Appl
18	47	60.3	28	5	US-10-928-926-53	Sequence 53, Appl
19	47	60.3	28	6	US-11-058-757-53	Sequence 53, Appl
20	47	60.3	28	6	US-11-185-907-35	Sequence 35, Appl
21	42	53.8	157	4	US-10-108-260A-3717	Sequence 3717, Ap
22	42	53.8	276	5	US-10-128-558-197	Sequence 197, App
23	42	53.8	342	4	US-10-156-761-12399	Sequence 12399, A
24	41	52.6	10	5	US-10-901-243-77	Sequence 77, Appl
25	41	52.6	10	5	US-10-901-243-78	Sequence 78, Appl
26	41	52.6	29	6	US-11-066-697-315	Sequence 315, App
27	41	52.6	29	6	US-11-066-697-328	Sequence 328, App
28	41	52.6	30	4	US-10-411-544-52	Sequence 52, Appl
29	41	52.6	30	6	US-11-066-697-310	Sequence 310, App
30	41	52.6	30	6	US-11-066-697-323	Sequence 323, App
31	41	52.6	31	3	US-09-813-345-18	Sequence 18, Appl
32	41	52.6	36	2	US-08-851-965-2	Sequence 2, Appli
33	41	52.6	36	2	US-08-851-965-30	Sequence 30, Appl
34	41	52.6	36	2	US-08-870-762A-7	Sequence 7, Appli
35	41	52.6	36	3	US-09-454-533-7	Sequence 7, Appli
36	41	52.6	36	4	US-10-649-138-7	Sequence 7, Appli
37	41	52.6	36	4	US-10-643-681-4	Sequence 4, Appli
38	41	52.6	36	5	US-10-991-597-12	Sequence 12, Appl
39	41	52.6	37	2	US-08-851-965-3	Sequence 3, Appli
40	41	52.6	37	2	US-08-851-965-29	Sequence 29, Appl
41	41	52.6	37	2	US-08-851-965-31	Sequence 31, Appl
42	41	52.6	37	2	US-08-851-965-32	Sequence 32, Appl
43	41	52.6	37	2	US-08-851-965-33	Sequence 33, Appl
44	41	52.6	37	2	US-08-870-762A-4	Sequence 4, Appli
45	41	52.6	37	2	US-08-870-762A-6	Sequence 6, Appli
46	41	52.6	37	2	US-08-870-762A-8	Sequence 8, Appli
47	41	52.6	37	2	US-08-870-762A-9	Sequence 9, Appli
48	41	52.6	37	2	US-08-870-762A-10	Sequence 10, Appl
49	41	52.6	37	3	US-09-813-345-16	Sequence 16, Appl
50	41	52.6	37	3	US-09-956-625-27	Sequence 27, Appl
51	41	52.6	37	3	US-09-454-533-1	Sequence 1, Appli
52	41	52.6	37	3	US-09-454-533-8	Sequence 8, Appli
53	41	52.6	37	3	US-09-454-533-34	Sequence 34, Appl
54	41	52.6	37	3	US-09-454-533-35	Sequence 35, Appl
55	41	52.6	37	3	US-09-454-533-36	Sequence 36, Appl
56	41	52.6	37	3	US-09-454-533-37	Sequence 37, Appl
57	41	52.6	37	3	US-09-454-533-41	Sequence 41, Appl
58	41	52.6	37	3	US-09-875-571A-1	Sequence 1, Appli
59	41	52.6	37	4	US-10-197-954-8	Sequence 8, Appli
60	41	52.6	37	4	US-10-301-488A-46	Sequence 46, Appl

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:15:15 ; Search time 34.4118 Seconds
 (without alignments)
 38.154 Million cell updates/sec

Title: US-10-749-522-21
 Perfect score: 78
 Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_AA:*

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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query					Description
No.	Score	Match	Length	DB	ID	
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1	78	100.0	15	2	US-09-830-954A-21	Sequence 21, Appl
2	47	60.3	28	2	US-09-724-961-53	Sequence 53, Appl
3	47	60.3	28	2	US-09-580-018-53	Sequence 53, Appl
4	47	60.3	28	2	US-09-724-551-53	Sequence 53, Appl
5	47	60.3	28	2	US-09-724-953-11	Sequence 11, Appl
6	47	60.3	28	2	US-09-724-567-11	Sequence 11, Appl
7	47	60.3	28	2	US-09-724-940-53	Sequence 53, Appl
8	47	60.3	28	2	US-09-979-952-11	Sequence 11, Appl
9	47	60.3	28	2	US-09-585-817-11	Sequence 11, Appl
10	44	56.4	34	1	US-07-927-755A-1	Sequence 1, Appl

11	44	56.4	34	1	US-07-927-755A-2	Sequence 2, Appli
12	41	52.6	11	7	5260275-2	Patent No. 5260275
13	41	52.6	20	1	US-07-794-288D-209	Sequence 209, App
14	41	52.6	29	2	US-09-623-548A-315	Sequence 315, App
15	41	52.6	29	2	US-09-623-548A-328	Sequence 328, App
16	41	52.6	29	2	US-09-657-276-315	Sequence 315, App
17	41	52.6	29	2	US-09-657-276-328	Sequence 328, App
18	41	52.6	30	1	US-07-794-288D-208	Sequence 208, App
19	41	52.6	30	2	US-09-813-345C-18	Sequence 18, Appli
20	41	52.6	30	2	US-09-623-548A-310	Sequence 310, App
21	41	52.6	30	2	US-09-623-548A-323	Sequence 323, App
22	41	52.6	30	2	US-09-657-276-310	Sequence 310, App
23	41	52.6	30	2	US-09-657-276-323	Sequence 323, App
24	41	52.6	30	7	5260275-4	Patent No. 5260275
25	41	52.6	31	2	US-09-070-504-18	Sequence 18, Appli
26	41	52.6	36	1	US-08-477-727A-79	Sequence 79, Appli
27	41	52.6	36	1	US-08-471-675A-5	Sequence 5, Appli
28	41	52.6	36	1	US-08-892-549-7	Sequence 7, Appli
29	41	52.6	36	2	US-08-302-069A-4	Sequence 4, Appli
30	41	52.6	36	2	US-09-576-062A-4	Sequence 4, Appli
31	41	52.6	36	2	US-09-454-533-7	Sequence 7, Appli
32	41	52.6	37	1	US-07-794-288D-1	Sequence 1, Appli
33	41	52.6	37	1	US-08-233-389C-10	Sequence 10, Appli
34	41	52.6	37	1	US-08-477-727A-80	Sequence 80, Appli
35	41	52.6	37	1	US-08-446-692-66	Sequence 66, Appli
36	41	52.6	37	1	US-08-471-675A-6	Sequence 6, Appli
37	41	52.6	37	1	US-08-259-762-1	Sequence 1, Appli
38	41	52.6	37	1	US-08-259-762-4	Sequence 4, Appli
39	41	52.6	37	1	US-08-259-762-5	Sequence 5, Appli
40	41	52.6	37	1	US-08-801-863-10	Sequence 10, Appli
41	41	52.6	37	1	US-08-486-596A-10	Sequence 10, Appli
42	41	52.6	37	1	US-08-488-351A-66	Sequence 66, Appli
43	41	52.6	37	1	US-09-004-713-10	Sequence 10, Appli
44	41	52.6	37	1	US-08-892-549-1	Sequence 1, Appli
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47	41	52.6	37	1	US-08-892-549-35	Sequence 35, Appli
48	41	52.6	37	1	US-08-892-549-36	Sequence 36, Appli
49	41	52.6	37	1	US-08-892-549-37	Sequence 37, Appli
50	41	52.6	37	1	US-08-892-549-41	Sequence 41, Appli
51	41	52.6	37	2	US-08-784-582-54	Sequence 54, Appli
52	41	52.6	37	2	US-08-302-069A-5	Sequence 5, Appli
53	41	52.6	37	2	US-09-070-504-16	Sequence 16, Appli
54	41	52.6	37	2	US-09-576-062A-5	Sequence 5, Appli
55	41	52.6	37	2	US-09-454-533-1	Sequence 1, Appli
56	41	52.6	37	2	US-09-454-533-8	Sequence 8, Appli
57	41	52.6	37	2	US-09-454-533-34	Sequence 34, Appli
58	41	52.6	37	2	US-09-454-533-35	Sequence 35, Appli
59	41	52.6	37	2	US-09-454-533-36	Sequence 36, Appli
60	41	52.6	37	2	US-09-454-533-37	Sequence 37, Appli

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:04:09 ; Search time 59.1176 Seconds
 (without alignments)
 116.010 Million cell updates/sec

Title: US-10-749-522-21
 Perfect score: 78
 Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

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1: geneseqp1980s:*

2: geneseqp1990s:*

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10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
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3	78	100.0	15	8	ADJ88127	Adj88127 Anti-aggr
4	47	60.3	28	4	AAB46176	Aab46176 Tetanus t
5	47	60.3	28	8	ADP02901	Adp02901 Fusion pr
6	47	60.3	28	9	AEA51392	Aea51392 Abeta and
7	47	60.3	28	9	AEA62803	Aea62803 Immunocon

8	47	60.3	28	9	AEC03768	Aec03768 A-beta 1-
9	47	60.3	28	10	AEF96798	Aef96798 Human amy
10	47	60.3	33	4	AAB49075	Aab49075 Amyloid b
11	42	53.8	157	7	ADM05032	Adm05032 Human pro
12	42	53.8	157	9	AEC87962	Aec87962 Human CDN
13	42	53.8	276	7	ADE08042	Ade08042 Novel pro
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16	41	52.6	10	2	AAW99230	Aaw99230 Amyloidog
17	41	52.6	10	2	AAY29577	Aay29577 Amylin am
18	41	52.6	10	7	ADF50817	Adf50817 Decamer p
19	41	52.6	10	7	ADF50818	Adf50818 Decamer p
20	41	52.6	10	8	ADR83633	Adr83633 Human IAP
21	41	52.6	10	8	ADR83634	Adr83634 Human IAP
22	41	52.6	10	9	ADV99064	Adv99064 Human IAP
23	41	52.6	10	9	ADV99065	Adv99065 Human IAP
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27	41	52.6	29	4	AAB91141	Aab91141 Pancreati
28	41	52.6	30	2	AAR37003	Aar37003 18His, 23
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34	41	52.6	30	4	AAB91136	Aab91136 Pancreati
35	41	52.6	30	7	ADM80671	Adm80671 Islet amy
36	41	52.6	31	4	AAE09822	Aae09822 Human amy
37	41	52.6	31	8	ADR83672	Adr83672 Amyloidog
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